

Figure 1

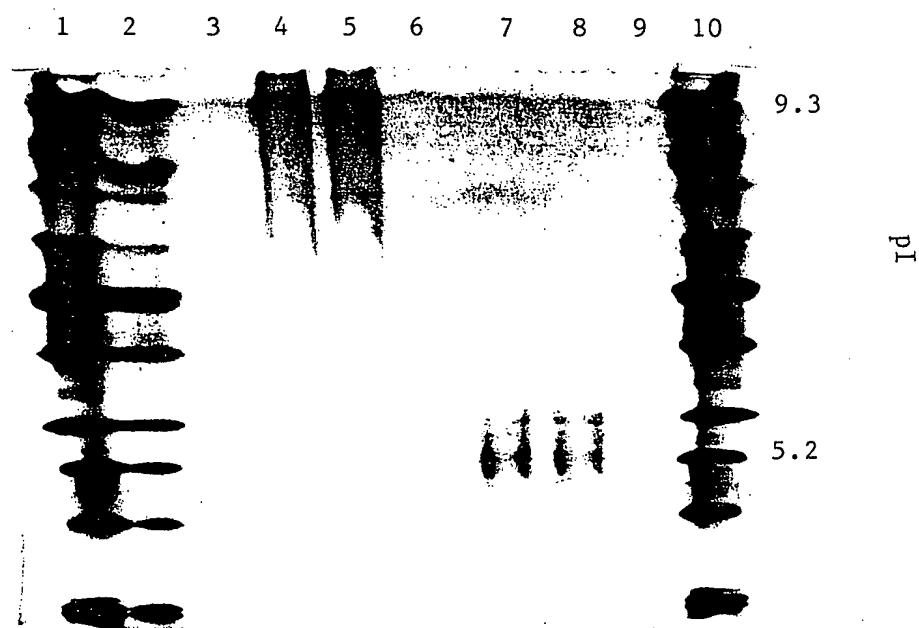


Figure 2

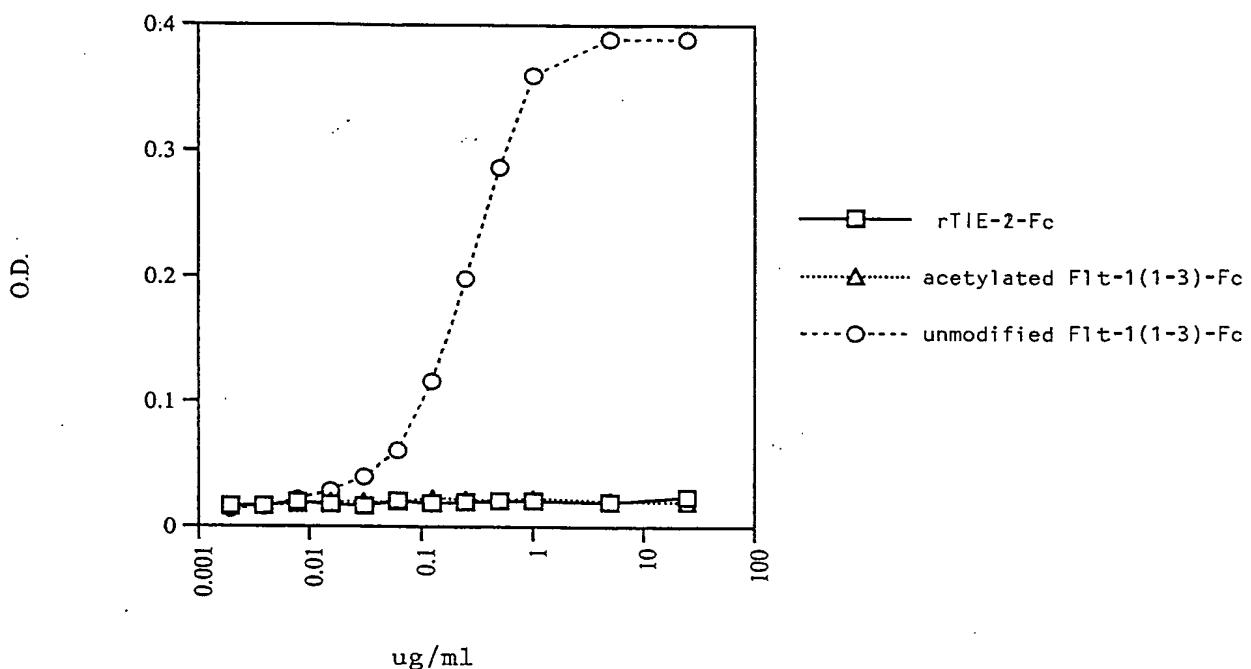


Figure 3

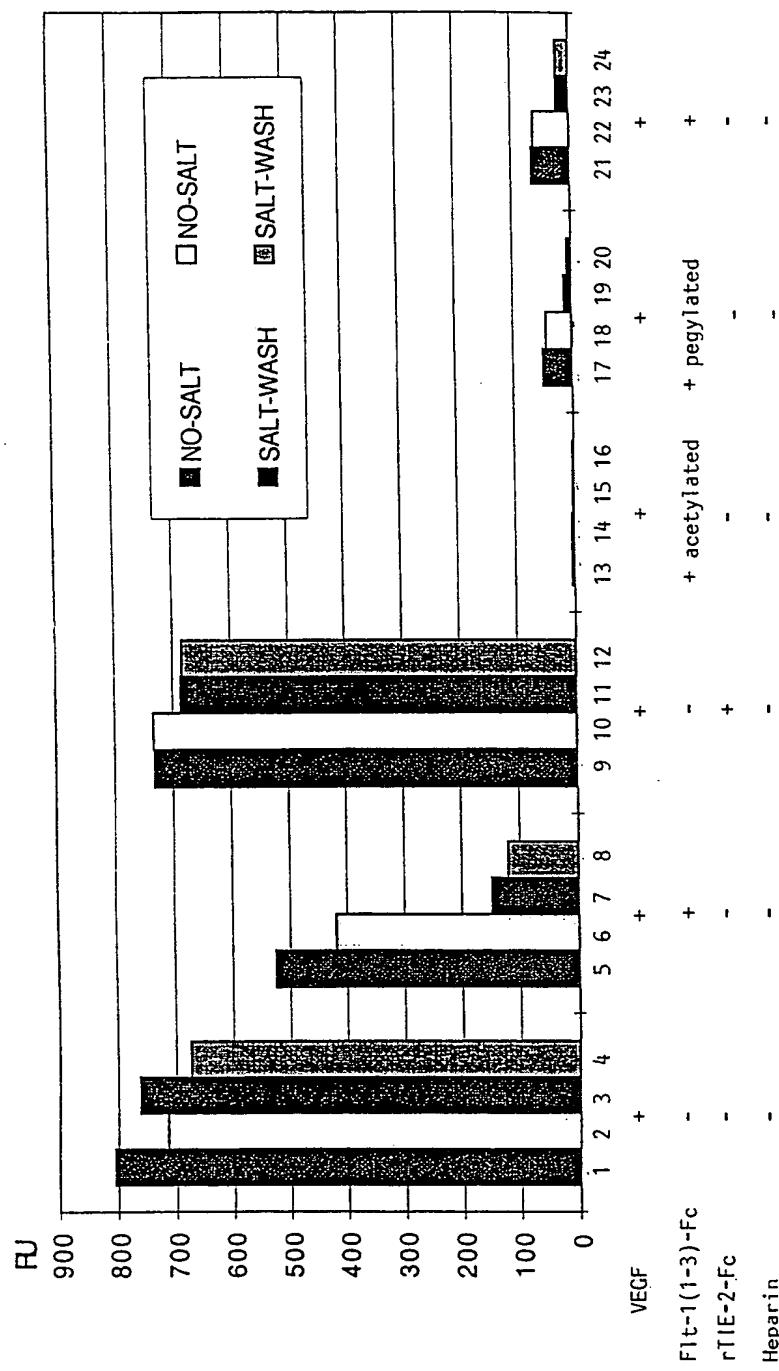


Figure 4

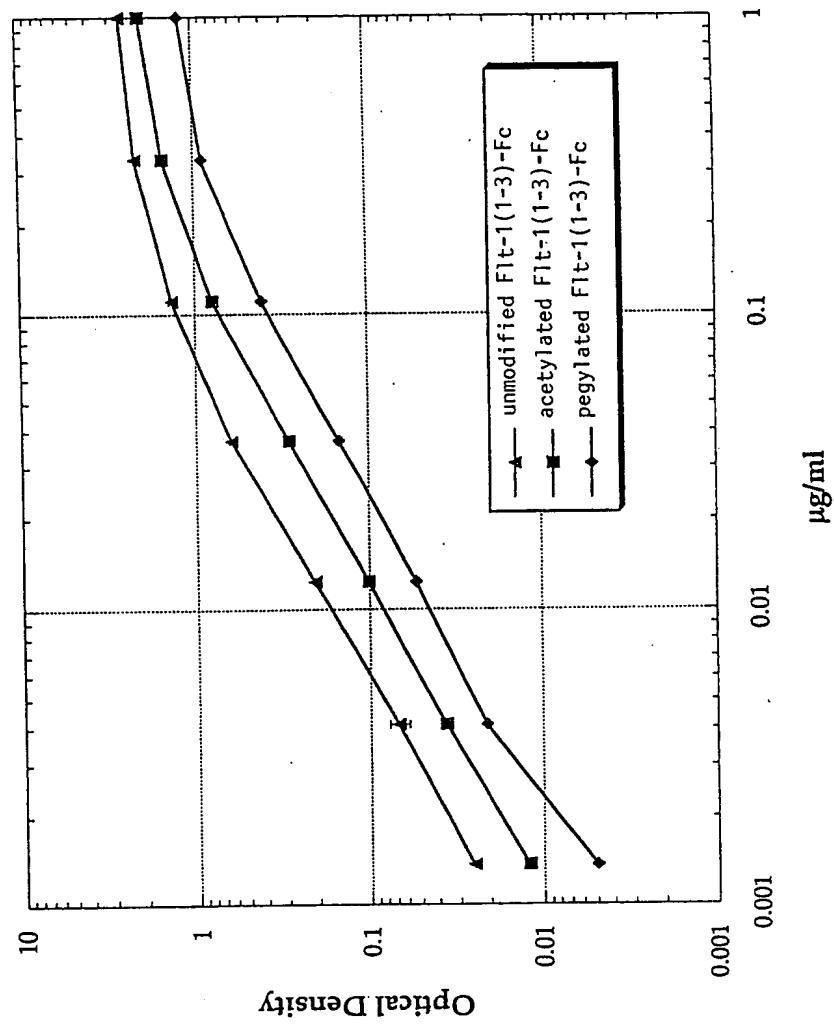


Figure 5

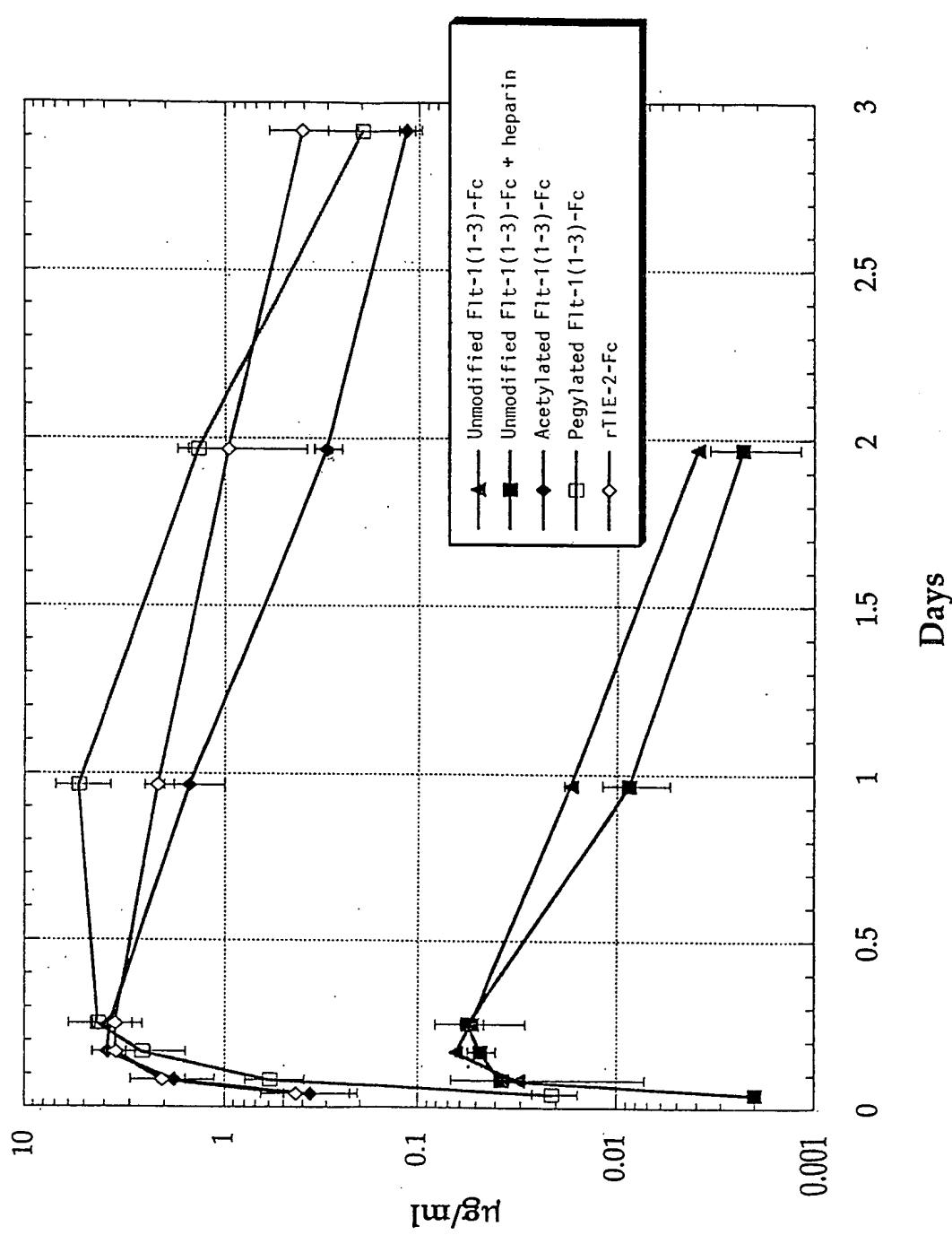


Figure 6A

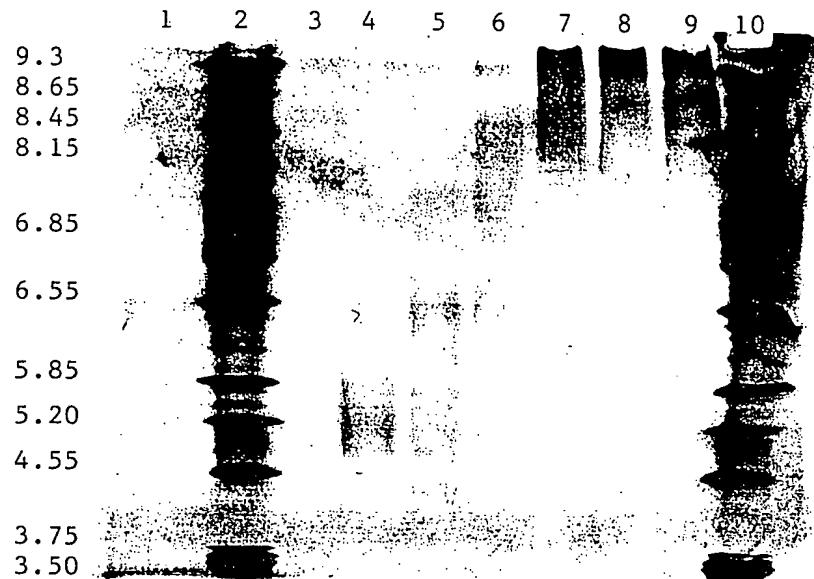


Figure 6B

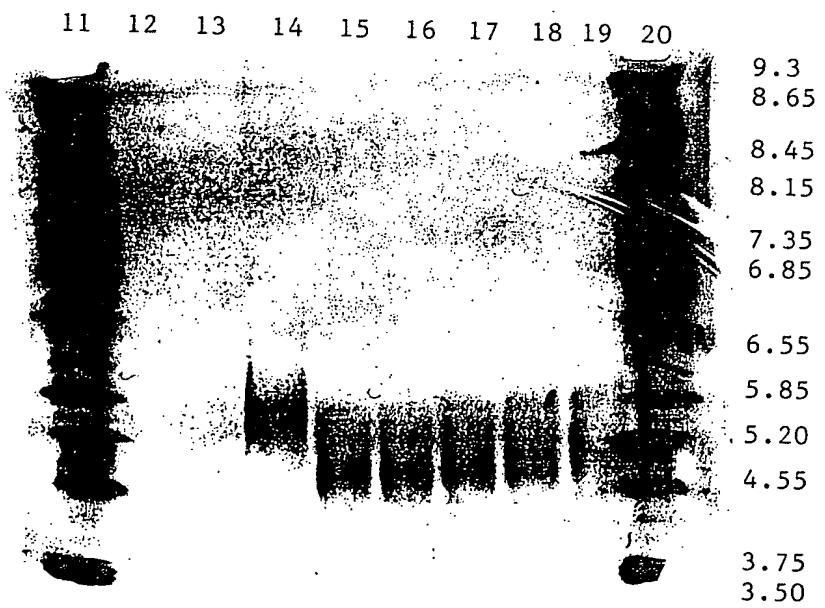


Figure 7

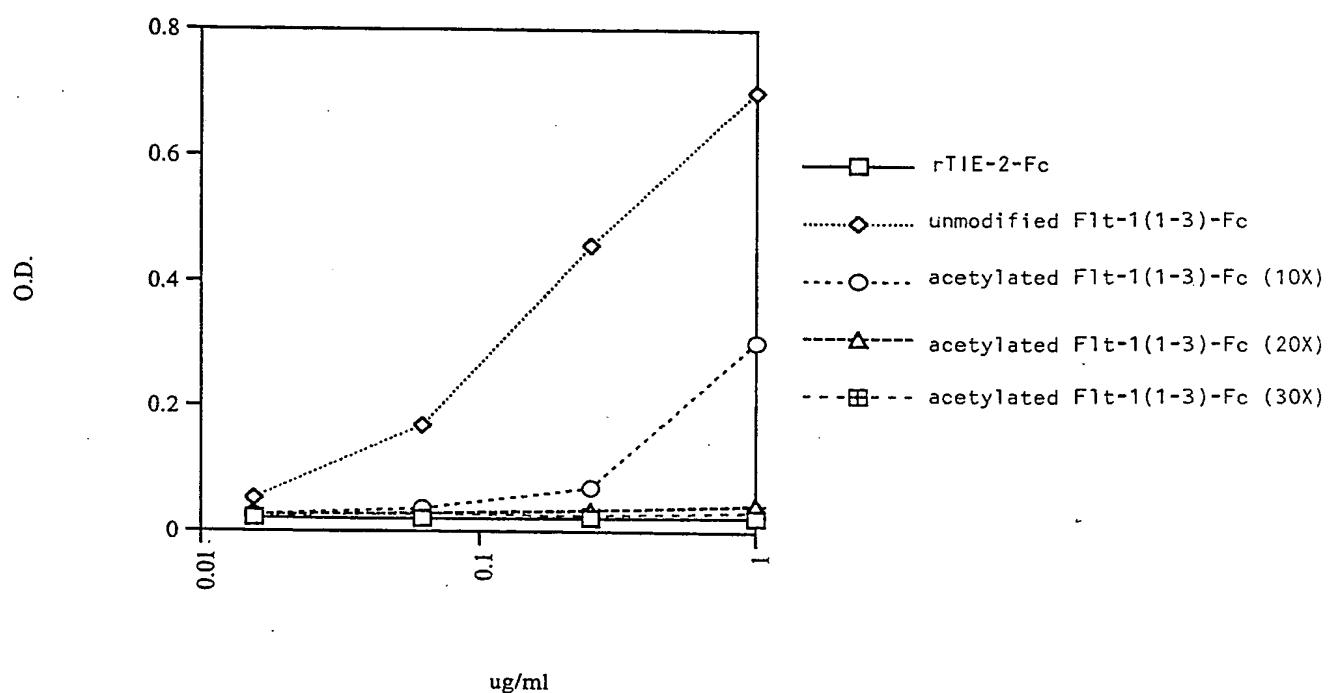


Figure 8

VEGF 0.2 ug/ml

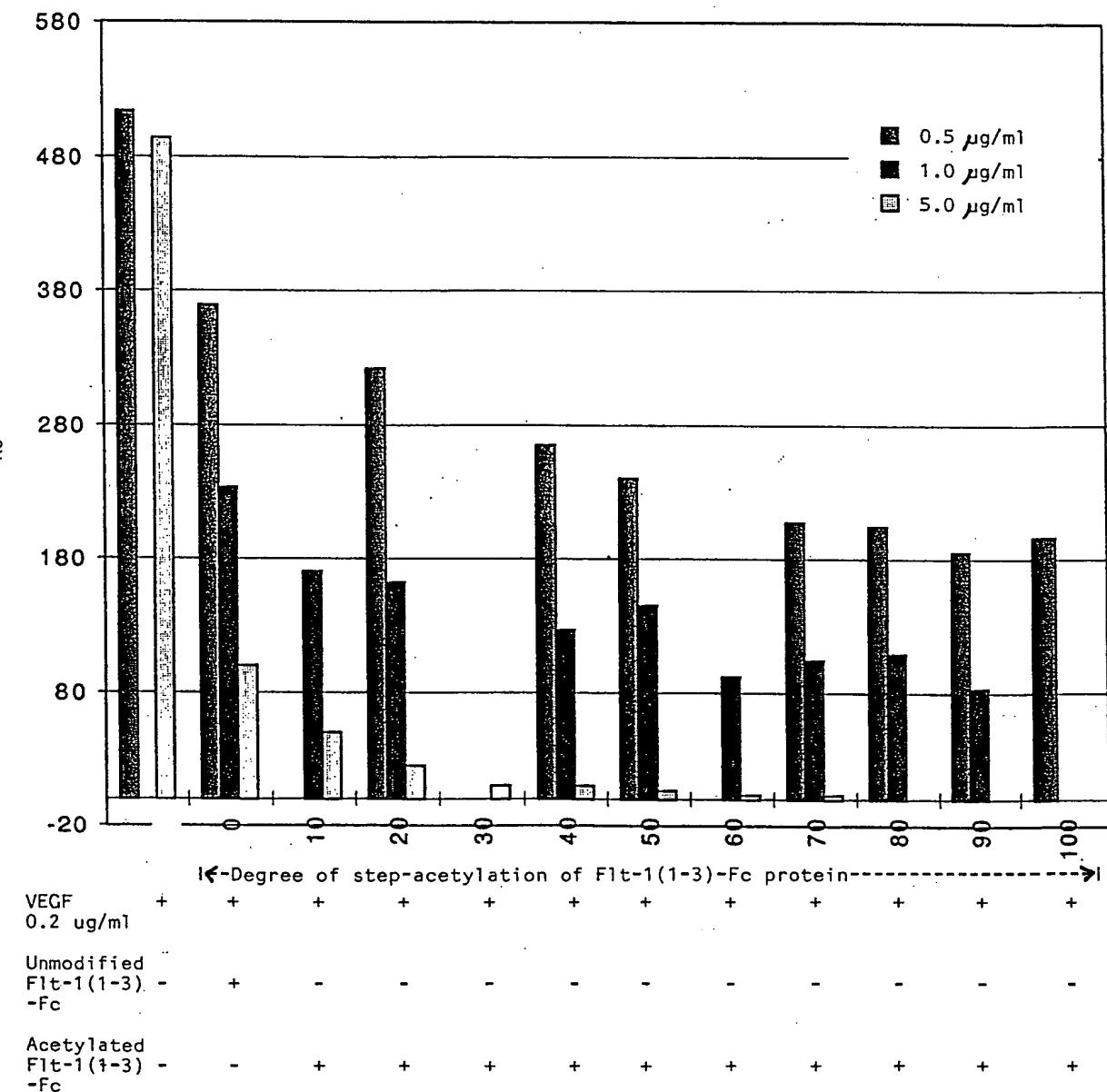


Figure 9

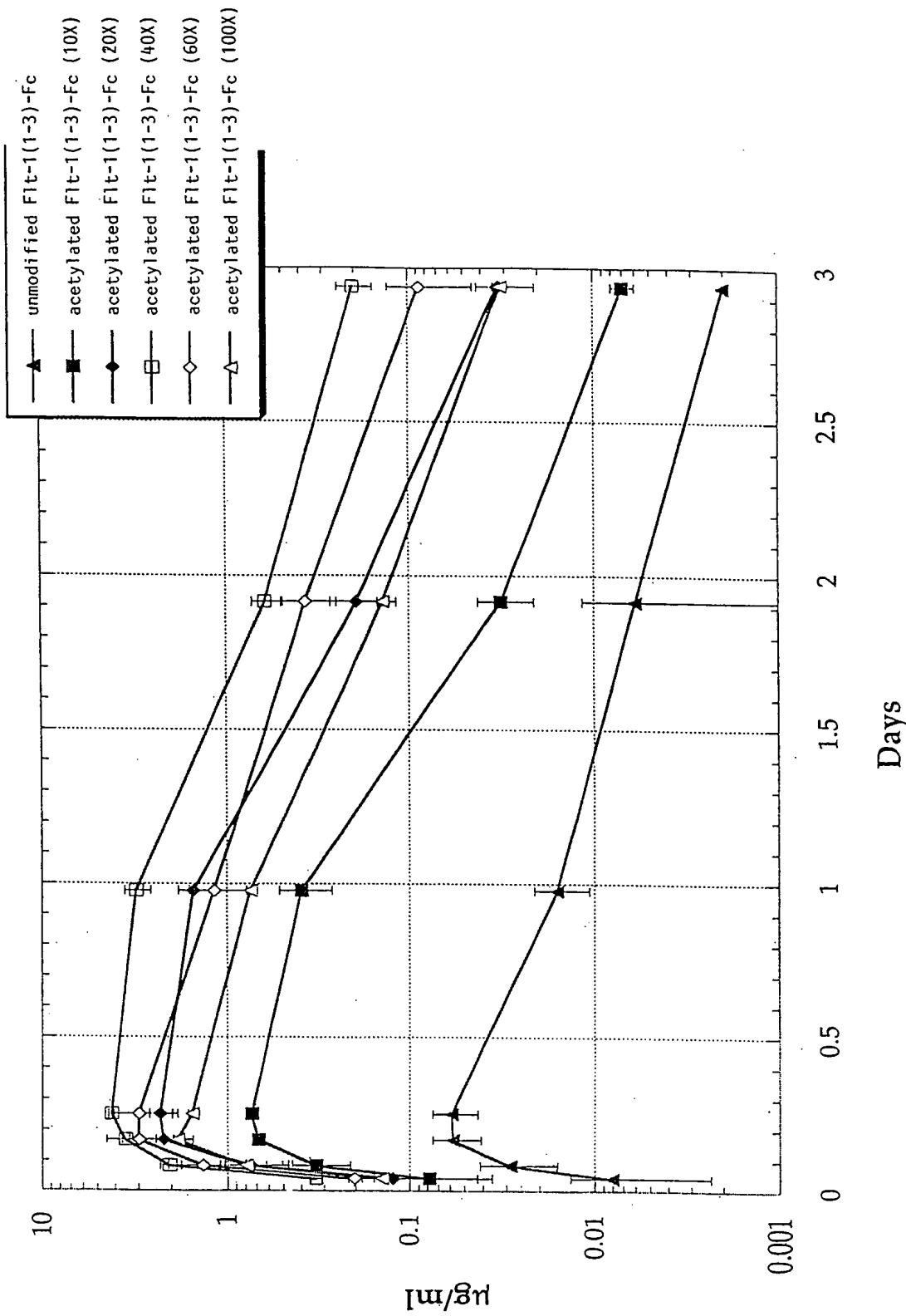


Figure 10A

TOTTEFO 2/26/2001

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC	TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG	Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>			
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG	TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC	Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>			
130	140	150	160	170	180
*	*	*	*	*	*
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA	GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT	His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>			
190	200	210	220	230	240
*	*	*	*	*	*
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC	ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG	Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>			
250	260	270	280	290	300
*	*	*	*	*	*
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC	ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG	Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>			
310	320	330	340	350	360
*	*	*	*	*	*
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTC CCT ACT TCA AAG AAG AAG GAA ACA	GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT	His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>			
370	380	390	400	410	420
*	*	*	*	*	*
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTC GAG ATG TAC AGT	CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA	Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>			
430	440	450	460	470	480
*	*	*	*	*	*
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT	CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACC GCC CAA	Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>			
490	500	510	520	530	540
*	*	*	*	*	*
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT	TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA	Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>			

Figure 10B

550 560 570 580 590 600
 * * * * * *
 GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
 CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
 Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

 610 620 630 640 650 660
 * * * * * *
 GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
 CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
 Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

 670 680 690 700 710 720
 * * * * * *
 CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
 GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
 Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

 730 740 750 760 770 780
 * * * * * *
 AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
 TTT AAT GAA TCT CCG GTPA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

 790 800 810 820 830 840
 * * * * * *
 AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA
 TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT
 Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg>

 850 860 870 880 890 900
 * * * * * *
 CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA
 GCT TAA CTG GTT TCG TTA AGG GTPA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT
 Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>

 910 920 930 940 950 960
 * * * * * *
 ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA
 TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT
 Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>

 970 980 990 1000 1010 1020
 * * * * * *
 TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT
 AGA CAA TTG TGG AGT CAC GTPA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA
 Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>

 1030 1040 1050 1060 1070 1080
 * * * * * *
 GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
 CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Pro Ser Val>

Figure 10C

1090 1100 1110 1120 1130 1140
 * * * * * * * * * * * *
 TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA
 AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>

 1150 1160 1170 1180 1190 1200
 * * * * * * * * * * * *
 TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC
 ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>

 1210 1220 1230 1240 1250 1260
 * * * * * * * * * * * *
 GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC
 CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>

 1270 1280 1290 1300 1310 1320
 * * * * * * * * * * * *
 CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG
 GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>

 1330 1340 1350 1360 1370 1380
 * * * * * * * * * * * *
 TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>

 1390 1400 1410 1420 1430 1440
 * * * * * * * * * * * *
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG
 CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>

 1450 1460 1470 1480 1490 1500
 * * * * * * * * * * * *
 AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG
 TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>

 1510 1520 1530 1540 1550 1560
 * * * * * * * * * * * *
 TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC
 ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>

 1570 1580 1590 1600 1610 1620
 * * * * * * * * * * * *
 GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG
 CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>

Figure 10D

1630 1640 1650 1660 1670 1680
* * * * * * * *
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

1690 1700
* * * *
CTC TCC CTG TCT CCG GGT AAA TGA
GAG AGG GAC AGA GGC CCA TTT ACT
Leu Ser Leu Ser Pro Gly Lys ***>

Figure 11

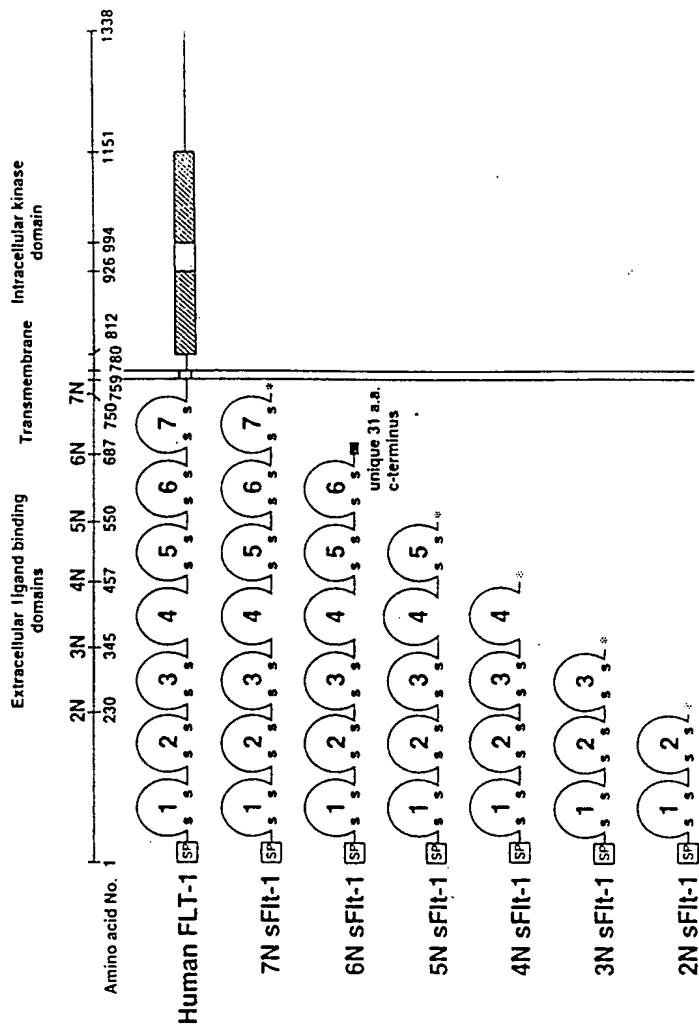


Figure 12A

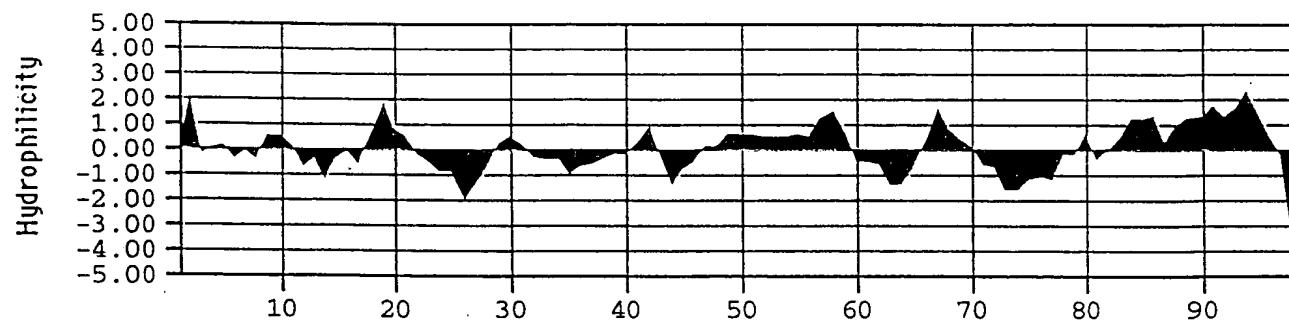


Figure 12B

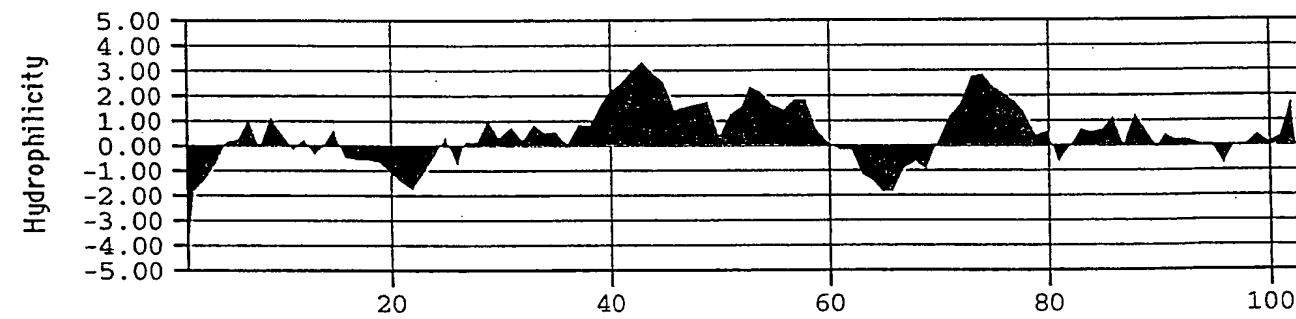


Figure 13A

10 20 30 40 50 60

* * * * *

ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC CGC GAC GAG TCG ACA GAC GAA GAG
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu>

70 80 90 100 110 120

* * * * *

ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GCC ACC CAG
TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC
Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>

130 140 150 160 170 180

* * * * *

CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA
GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT
His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>

190 200 210 220 230 240

* * * * *

TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC
ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG
Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>

250 260 270 280 290 300

* * * * *

TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC
ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Asn Thr Ala Gln Ala Asn>

310 320 330 340 350 360

* * * * *

CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA
GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT
His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>

370 380 390 400 410 420

* * * * *

GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT
CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA
Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>

430 440 450 460 470 480

* * * * *

GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT
CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA
Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>

490 500 510 520 530 540

* * * * *

ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT
TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA
Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>

Figure 13B

550 560 570 580 590 600
 * * * * * * * * * * * *
 GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
 CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
 Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

 610 620 630 640 650 660
 * * * * * * * * * * * *
 GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
 CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
 Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

 670 680 690 700 710 720
 * * * * * * * * * * * *
 CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
 GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
 Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

 730 740 750 760 770 780
 * * * * * * * * * * * *
 AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
 TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

 790 800 810 820 830 840
 * * * * * * * * * * * *
 AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC
 TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG
 Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn>

 850 860 870 880 890 900
 * * * * * * * * * * * *
 ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT
 TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA
 Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr>

 910 920 930 940 950 960
 * * * * * * * * * * * *
 TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT
 ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA
 Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp>

 970 980 990 1000 1010 1020
 * * * * * * * * * * * *
 AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA
 TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT AGC GGT GGC ACG GGT
 Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro>

 1030 1040 1050 1060 1070 1080
 * * * * * * * * * * * *
 GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG
 Ala Pro Glu Leu Leu Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Asp Thr>

Figure 13C

1090 1100 1110 1120 1130 1140
 * * * * * * * * * * * *
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC
 GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CTC CAC TCG CAC TCG GTG CTT CTG
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp>

 1150 1160 1170 1180 1190 1200
 * * * * * * * * * * * *
 CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
 GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTC TTA CGG TTC TGT TTC
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys>

 1210 1220 1230 1240 1250 1260
 * * * * * * * * * * * *
 CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC
 GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His>

 1270 1280 1290 1300 1310 1320
 * * * * * * * * * * * *
 CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC
 GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG CAG AGG TTG TTT CGG GAG GGT CGG
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala>

 1330 1340 1350 1360 1370 1380
 * * * * * * * * * * * *
 CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC
 GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr>

 1390 1400 1410 1420 1430 1440
 * * * * * * * * * * * *
 CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA
 GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys>

 1450 1460 1470 1480 1490 1500
 * * * * * * * * * * * *
 GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC
 CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn>

 1510 1520 1530 1540 1550 1560
 * * * * * * * * * * * *
 TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGG TCC TTC TTC CTC TAC AGC AAG CTC
 ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu>

 1570 1580 1590 1600 1610 1620
 * * * * * * * * * * * *
 ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTC CTC
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu>

Figure 13D

1630	1640	1650	1660	1670													
*	*	*	*	*													
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA
CGA	GAC	GTG	TTG	GTG	ATG	TGC	GTC	TTC	TCG	GAG	AGG	GAC	AGA	GGC	CCA	TTT	ACT
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	****>

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Figure 14A

10 20 30 40 50 60

* * * * * * * * *

ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC CGC GAC GAG TCG ACA GAC GAA GAG
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

70 80 90 100 110 120

* * * * * * * * *

ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT
TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA
Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>

130 140 150 160 170 180

* * * * * * * * *

ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC
TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG
Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>

190 200 210 220 230 240

* * * * * * * * *

ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC
TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG
Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>

250 260 270 280 290 300

* * * * * * * * *

TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG
ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CCT TAT CCC GAA GAC
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>

310 320 330 340 350 360

* * * * * * * * *

ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA
TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT
Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>

370 380 390 400 410 420

* * * * * * * * *

ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC
TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT CGC TTT AAT GAA TCT CCG
Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>

430 440 450 460 470 480

* * * * * * * * *

CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC
GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG
His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>

490 500 510 520 530 540

* * * * * * * * *

TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT
ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA
Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val>

Figure 14B

550 * * * * 560 * * * * 570 * * * * 580 * * * * 590 * * * * 600 * * * *
 CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT
 GAA TGA TAA CTG TTT TAC GTC TTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA
 Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser>

 610 * * * * 620 * * * * 630 * * * * 640 * * * * 650 * * * * 660 * * * *
 GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC
 CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG
 Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly>

 670 * * * * 680 * * * * 690 * * * * 700 * * * * 710 * * * * 720 * * * *
 GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG
 CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACC GGT CGT GGA CTT GAG GAC
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu>

 730 * * * * 740 * * * * 750 * * * * 760 * * * * 770 * * * * 780 * * * *
 GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CCG
 CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg>

 790 * * * * 800 * * * * 810 * * * * 820 * * * * 830 * * * * 840 * * * *
 ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC
 TGG GGA CTC CAG TGT ACG CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG
 Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe>

 850 * * * * 860 * * * * 870 * * * * 880 * * * * 890 * * * * 900 * * * *
 AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG
 TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln>

 910 * * * * 920 * * * * 930 * * * * 940 * * * * 950 * * * * 960 * * * *
 TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT
 ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn>

 970 * * * * 980 * * * * 990 * * * * 1000 * * * * 1010 * * * * 1020 * * * *
 GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC
 CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr>

 1030 * * * * 1040 * * * * 1050 * * * * 1060 * * * * 1070 * * * * 1080 * * * *
 ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG
 TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg>

Figure 14C

1090 1100 1110 1120 1130 1140
 * * * * * * * * * * * *
 GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC
 CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser>

 1150 1160 1170 1180 1190 1200
 * * * * * * * * * * *
 GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT
 CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro>

 1210 1220 1230 1240 1250 1260
 * * * * * * * * * * *
 CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC
 GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser>

 1270 1280 1290 1300 1310 1320
 * * * * * * * * * * *
 AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC
 TCC ACC GTC GTC CCC TTG CAG AAG AGT ACC AGG CAC TAC GTC CTC CGA GAC GTG TTG GTG
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His>

 1330 1340 1350
 * * * * * * *
 TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
 ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>

1070 1071 1072 1073 1074 1075 1076 1077 1078 1079

Figure 15A

10 20 30 40 50 60
 * * * * * * * * * * * * * *
 ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
 TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

 70 80 90 100 110 120
 * * * * * * * * * * * * * *
 ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT
 TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA
 Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>

 130 140 150 160 170 180
 * * * * * * * * * * * * * *
 ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC
 TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG
 Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>

 190 200 210 220 230 240
 * * * * * * * * * * * * * *
 ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC
 TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG
 Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>

 250 260 270 280 290 300
 * * * * * * * * * * * * * *
 TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG
 ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC
 Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>

 310 320 330 340 350 360
 * * * * * * * * * * * * * *
 ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA
 TGG ACA CTT CGT TGT CAG TTA CCC GTC AAC ATA TTC TGT TTG ATA GAG TGT GTC GCT GTT
 Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>

 370 380 390 400 410 420
 * * * * * * * * * * * * * *
 ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC
 TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG
 Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>

 430 440 450 460 470 480
 * * * * * * * * * * * * * *
 CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC
 GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG
 His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>

 490 500 510 520 530 540
 * * * * * * * * * * * * * *
 TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA CGA ATT GAC CAA AGC
 ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT GCT TAA CTG GTT TCG
 Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser>

Figure 15B

TOP SECRET//COMINT

550	560	570	580	590	600
*	*	*	*	*	*
AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp>					
610	620	630	640	650	660
*	*	*	*	*	*
AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser>					
670	680	690	700	710	720
*	*	*	*	*	*
GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT Val His Ile Tyr Asp Lys Ala Gly Pro Gly Pro Lys Ser Cys Asp Lys Thr His Thr>					
730	740	750	760	770	780
*	*	*	*	*	*
TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro>					
790	800	810	820	830	840
*	*	*	*	*	*
AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>					
850	860	870	880	890	900
*	*	*	*	*	*
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTC Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His>					
910	920	930	940	950	960
*	*	*	*	*	*
AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val>					
970	980	990	1000	1010	1020
*	*	*	*	*	*
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn>					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>					

Figure 15C

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Figure 16A

10	20	30	40	50	60
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC	TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG	Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>	*	*	*
70	80	90	100	110	120
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG	TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC	Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>	*	*	*
130	140	150	160	170	180
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA	GTG TAG TAC GTT CGT CCG GTC TGT GAC GTÀ GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT	His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>	*	*	*
190	200	210	220	230	240
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC	ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG	Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>	*	*	*
250	260	270	280	290	300
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC	ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG	Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>	*	*	*
310	320	330	340	350	360
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA	GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT	His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>	*	*	*
370	380	390	400	410	420
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT	CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA	Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>	*	*	*
430	440	450	460	470	480
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT	CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACC GCC CAA	Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>	*	*	*
490	500	510	520	530	540
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT	TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA	Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>	*	*	*

Figure 16B

550 560 570 580 590 600

* * * * * *

GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

610 620 630 640 650 660

* * * * * *

GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

670 680 690 700 710 720

* * * * * *

CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

730 740 750 760 770 780

* * * * * *

AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

790 800 810 820 830 840

* * * * * *

AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AAC GCT TCC GTA AGG CGA
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TTG CGA AGG CAT TCC GCT
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Ala Ser Val Arg Arg>

850 860 870 880 890 900

* * * * * *

CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA
GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT
Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>

910 920 930 940 950 960

* * * * * *

ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA
TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT
Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>

970 980 990 1000 1010 1020

* * * * * *

TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT
AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>

1030 1040 1050 1060 1070 1080

* * * * * *

GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Pro Ser Val>

Figure 16C

TOP SECRET//~~REF ID: A650~~

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CCG ACC CCT GAG GTC ACA AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>					
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>					
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>					
1390	1400	1410	1420	1430	1440
*	*	*	*	*	*
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>					
1450	1460	1470	1480	1490	1500
*	*	*	*	*	*
AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>					
1510	1520	1530	1540	1550	1560
*	*	*	*	*	*
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>					
1570	1580	1590	1600	1610	1620
*	*	*	*	*	*
GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>					

Figure 16D

1630 1640 1650 1660 1670 1680
* * * * * * * *
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

1690 1700
* * * *
CTC TCC CTG TCT CCG GGT AAA TGA
GAG AGG GAC AGA GGC CCA TTT ACT
Leu Ser Leu Ser Pro Gly Lys ***>

0 1 2 3 4 5 6 7 8 9

Figure 17

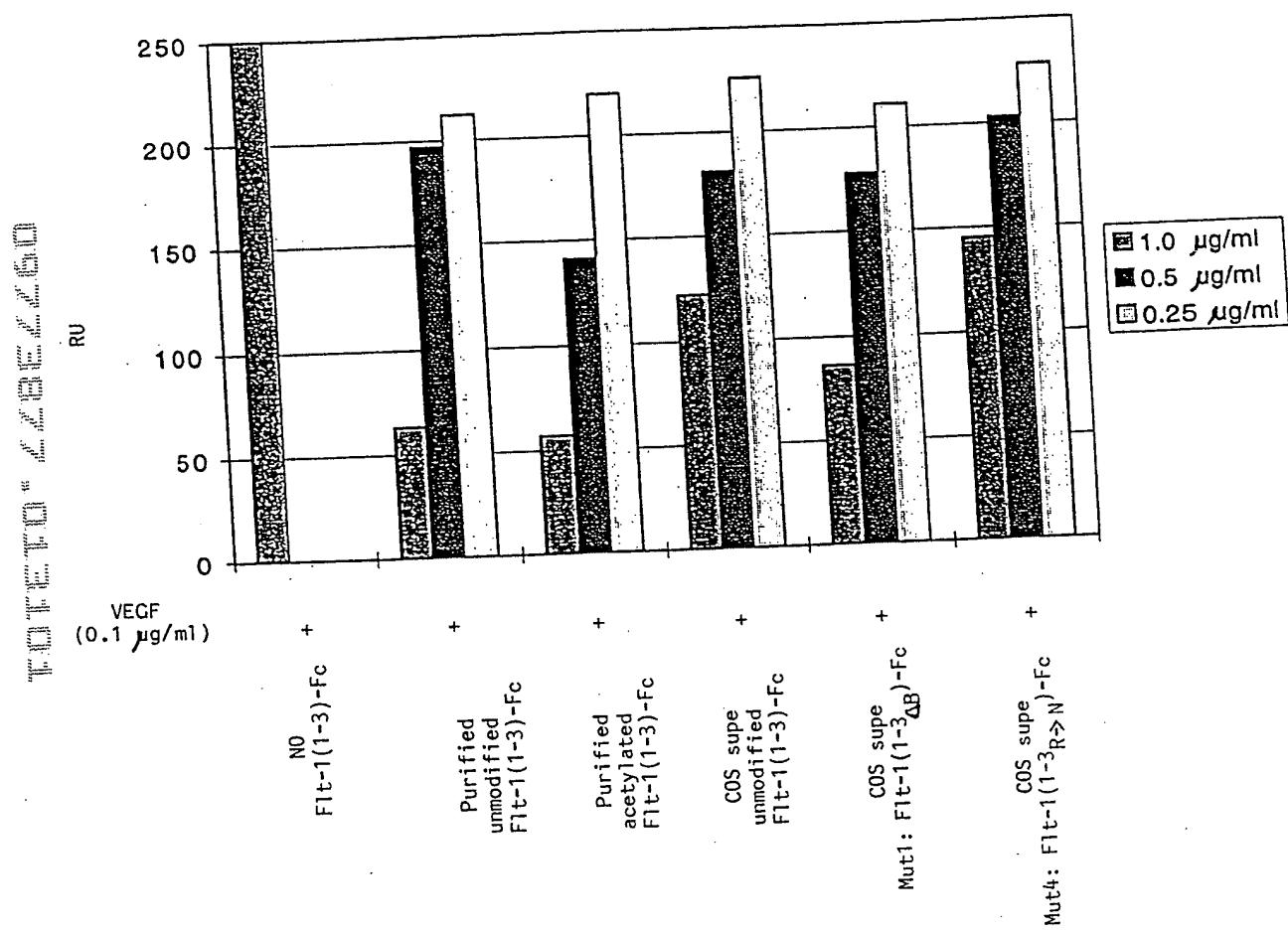


Figure 18

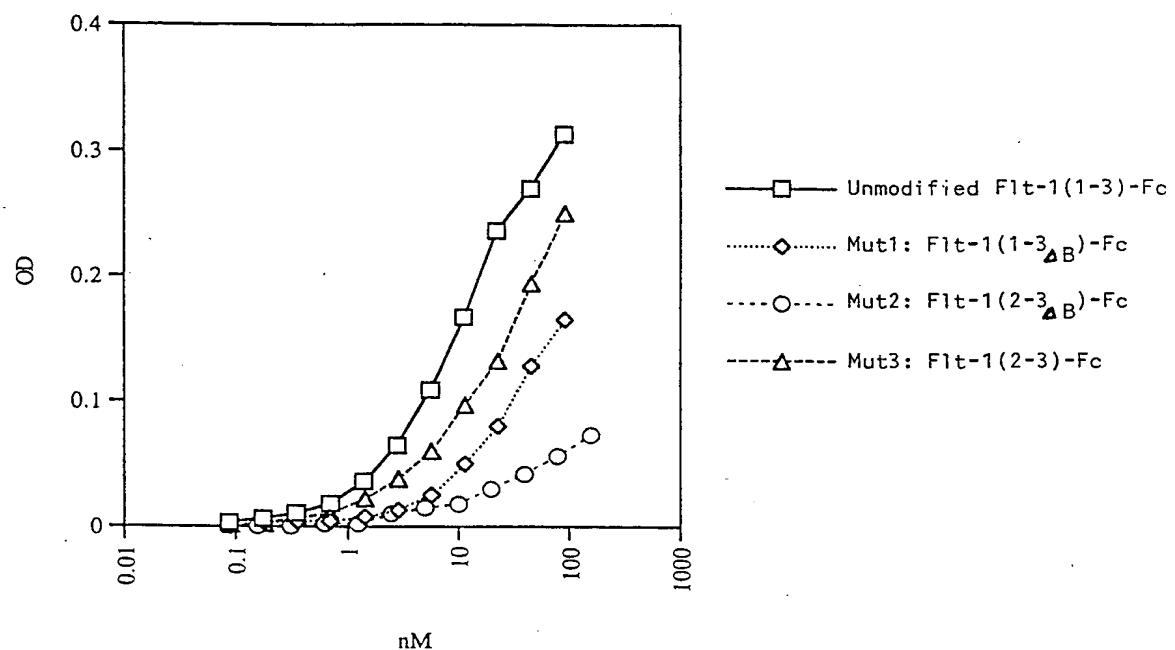


Figure 19

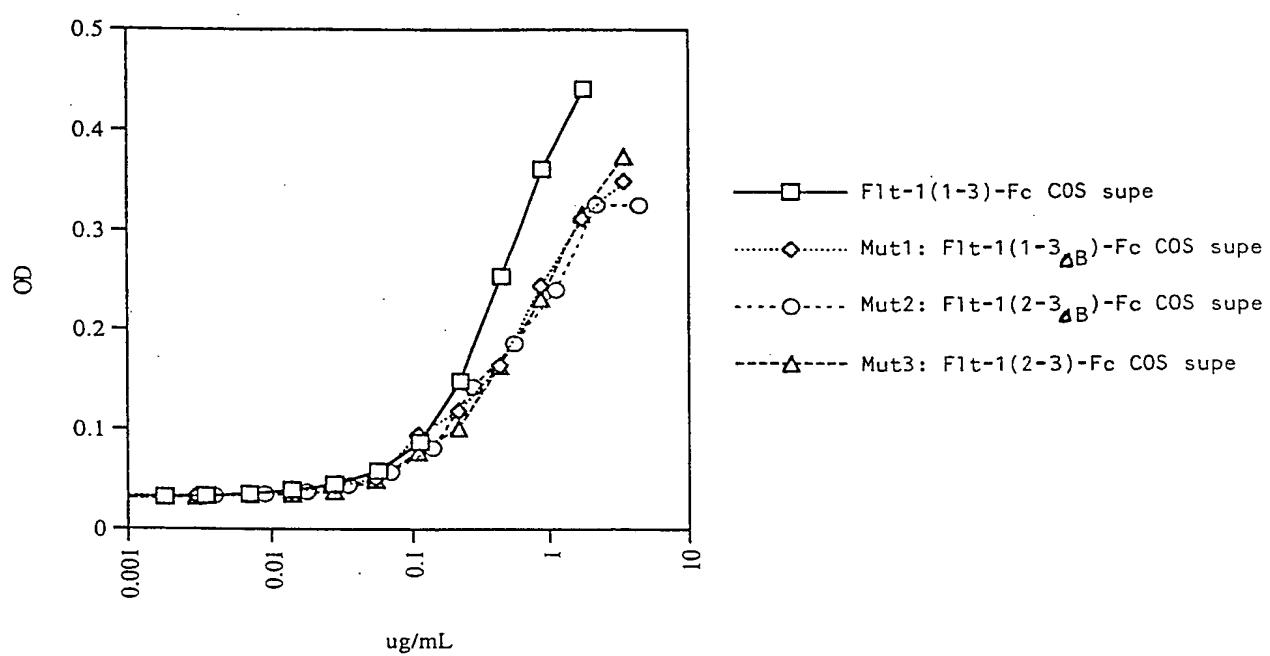


Figure 20

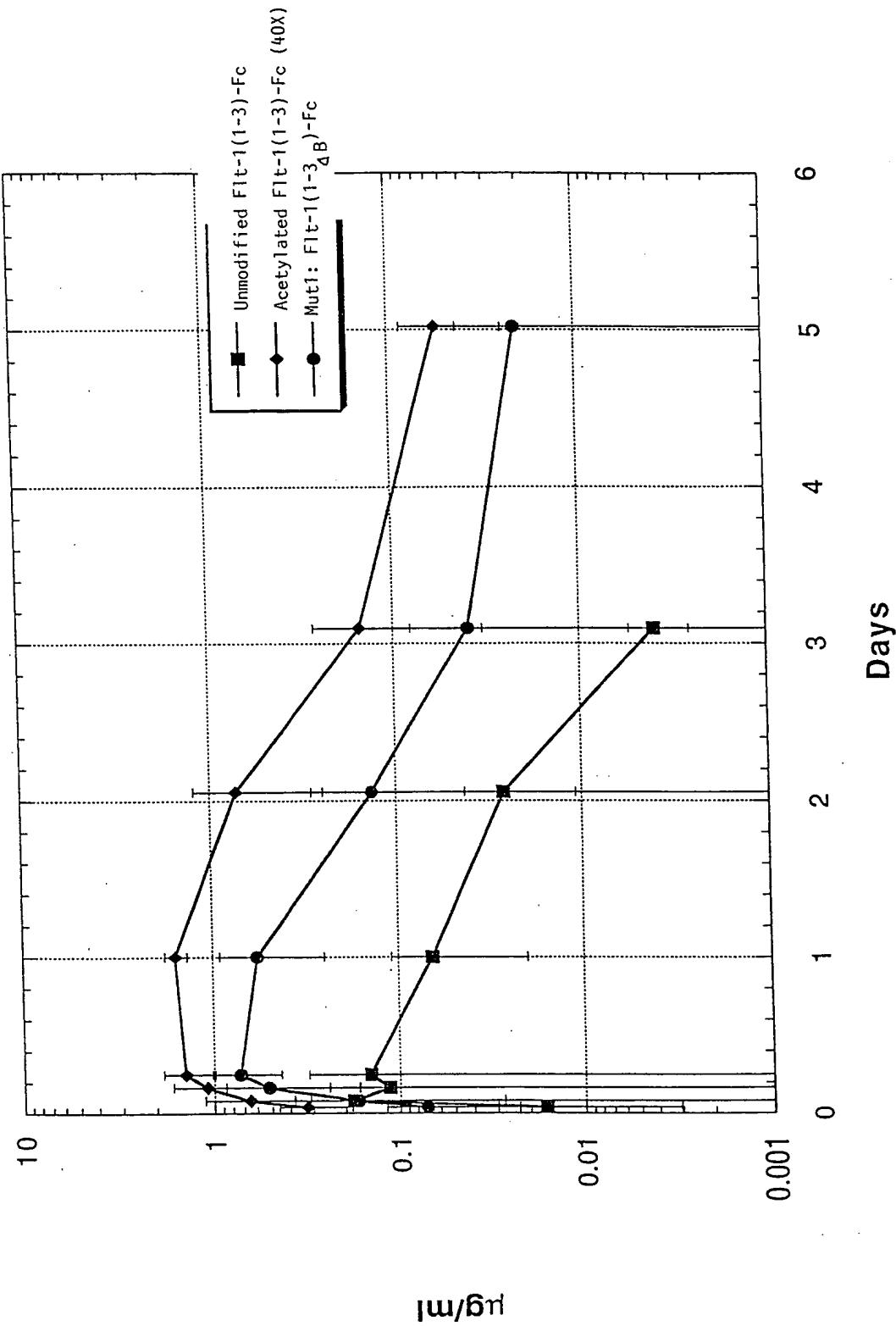


Figure 21A

>EcoRI_site

10	20	30	40	50	60	70	80
AAGCTTGGGCTGCAGGTCGATCGACTCTAGAGGATCGATCCCCGGGAGCTCGAATTGCAACCACCATGGTCAGCTAC							
TTCGAACCCGACGTCCAGCTAGCTGAGATCTCCTAGCTAGGGGCCGCTGAGCTTAAGCGTTGGTGGTACCAAGTCGATG							
M	V	S	Y>				
1				4			

>

>BspEI_bridge

90	100	110	120	130	140	150	160
TGGGACACCGGGGTCCTGCTGCGCGCTGCTCAGCTGCTGCTTCACAGGATCTAGTTCCGGAGGTAGACCTTTCGT							
ACCCCTGTGGCCCCAGGACGACACGCGCGACGAGTCGACAGACGAAGAGTGTCTAGATCAAGGCCTCCATCTGGAAAGCA							
W	D	T	G	V	L	L	C
A L L S C L L L T G S S >							
FLT1 SS >							
S G >							
>							
G	R	P	F	V>			
31							

>

170 180 190 200 210 220 230 240

AGAGATGTACAGTCAAATCCCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTAC

TCTCTACATGTCACTTAGGGCTTAAATATGTGTACTGACTTCCCTCGAGCAGTAAGGGACGGCCCAATGCAGTG

E M Y S E I P E I I H M T E G R E L V I P C R V T S >

57.

HFLT1 D2 >

250 260 270 280 290 300 310 320

CTAACATCACTGTTACTTTAAAAAGTTCCACTTGACACTTGATGCCCTGATGGAAAACGCATAATCTGGGACAGTAGA

GATTGTAGTGACAATGAAATTTCAAAGGTGAAGTGTGAAACTAGGGACTACCTTTGCGTATTAGACCCCTGTCATCT

P N I T V T L K K F P L D T L I P D G K R I I W D S R >

84.

HFLT1 D2 >

330 340 350 360 370 380 390 400

AAGGGCTTCATCATCAAATGCAACGTACAAAGAAATAGGGCTCTGACCTGTGAAGCAACAGTCATGGCATTGTA

TTCCCGAAGTAGTATAGTTACGTTGCACTGTTCTTATCCCGAAGACTGGACACTCGTGTCAAGTACCCGTAAACAT

K G F I I S N A T Y K E I G L L T C E A T V N G H L Y >

111.

HFLT1 D2 >

410 420 430 440 450 460 470 480

TAAGACAAACTATCTCACACATCGACAAACCAATACAATCATAGATGTGGTCTGAGTCCGTCATGAAATTGAACAT

ATTCTGTTGATAGAGTGTGTAGCTGTTGGTTATGTTAGTATCTACACCAAGACTCAGGCAGAGTACCTAACCTGATA

K T N Y L T H R Q T N T I I D >

HFLT1 D2 >

V V L S P S H G I E L >

137.

HFLK1 D3 >

Figure 21B

PROTEIN: 228E22610

490 500 510 520 530 540 550 560
 CTGTTGGAGAAAAGCTTGTCTAAATTGTACAGCAAGAACCTGAACCTAAATGTGGGGATTGACTTCACACTGGGAATACCCCT
 GACAACCTCTTTCGAACAGAATTAAACATGCGTCTGACTTGATTTACACCCCTAACGTTGACCCCTTATGGGA
 S V G E K L V L N C T A R T E L N V G I D F N W E Y P>
 164
 HFLK1 D3 >

570 580 590 600 610 620 630 640
 TCTTCGAAGCATCAGCATAAGAACCTGTAAACCGAGACCTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGAG
 AGAACGCTTCGTAGTCGTATTCTTGAAACATTGGCTCTGGATTTGGTCAGACCCCTACTCTACTTCTTAAACACTC
 S S K H Q H K K L V N R D L K T Q S G S E M K K F L S>
 191
 HFLK1 D3 >

650 660 670 680 690 700 710 720
 CACCTTAACCTAGATGGTGTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGCTGATGACCAAGA
 GTGGAATTGATATCTACCACATTGGGCCTCACTGGTCTAACATGGACACGTCGTAGGTACCCGACTACTGGTCT
 T L T I D G V T R S D Q G L Y T C A A S S S G L M T K>
 217
 HFLK1 D3 >

>Srf_Bridge_

730 740 750 | 760 770 780 790 800
 AGAACAGCACATTGTCAGGGTCCATGAAAAGGGCCCGGCGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAA
 TCTTGTGTTGAAACAGTCCCAGGTACTTTCCCGGGCCGCTGTTTGAGTGTGACGGTGGCACGGGTCTGGACTT
 K N S T F V R V H E K>
 HFLK1 D3 >

G P G>

D K T H T C P P C P A P E>
244

FCΔC1 (A) >

810 820 830 840 850 860 870 880
 CTCCCTGGGGGGACCGTCAGTCTTCCCTTCCCCCCTAAACCCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTAC
 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCTGGGACTCCAGTG
 L L G G P S V F L F P P K P K D T L M I S R T P E V T>
 271
 FCΔC1 (A) >

890 900 910 920 930 940 950 960
 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGGACGGCGTGGAGGTGCATAATG
 TACGCACCAACCACCTGCACTCGGTCTCTGGGACTCCAGTTCAAGTGTGACCATGCACCTGCCACCTCCACGTATTAC
 C V V V D V S H E D P E V K F N W Y V D G V E V H N>
 297
 FCΔC1 (A) >

970 980 990 1000 1010 1020 1030 1040
 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTCACCGTCTGCACCCAGTGCAGGAGTGGCAGGACGTGGTCTGACC
 GGTTCTGTTTGGGCCCTCCTCGTCATGTTGCGTCATGGCACACCAGTGCAGGAGTGGCAGGACGTGGTCTGACC
 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W>
 324
 FCΔC1 (A) >

Figure 21C

1050 1060 1070 1080 1090 1100 1110 1120
 CTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAA
 GACTTACCGTTCCCTATGTTACAGTTCCAGAGGTTGTTGGGAGGGTAGCTCTTGGTAGAGGTTTCGGTT
 L N G K E Y K C K V S N K A L P A P I E K T I S K A K>
 351
 FCΔC1 (A) _____>

>A>C_A_allotype
 |
 >G>T_A_allotype
 |
 1130 1140 1150 1160 1170 1180 1190 1200
 AGGGCAGCCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCGGGATGAGCTGACCAAGAACAGGTCAAGCTGACCT
 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGACGGGGTAGGGCCCTACTCGACTGGTCTGGTCCAGTCGGACTGGA
 G Q P R E P Q V Y T L P P S R D E L T K N Q V S L T>
 377
 FCΔC1 (A) _____>

1210 1220 1230 1240 1250 1260 1270 1280
 GCCTGGTCAAAGGCTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACC
 CGGACCACTTTCCGAAGATAAGGTCGCTGTAGCGGCACCTCACCCCTCTCGTTACCCGTCGGCTCTGGTIGATGTTCTGG
 C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T>
 404
 FCΔC1 (A) _____>

>T>C
 |
 1290 1300 1310 1320 1330 1340 1350 1360
 ACGCCTCCCGTGTGGACTCCGACGGCTCCTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATATCGTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC
 T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G>
 431
 FCΔC1 (A) _____>

1370 1380 1390 1400 1410 1420 1430 1440
 GAACGTCTTCTATGCTCCGTATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCTGGGTA
 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGGTATGCGTCTCGGAGAGGGACAGAGGCCAT
 N V F S C S V M H E A L H N H Y T Q K S L S L S P G>
 457
 FCΔC1 (A) _____>

>NotI_site
 |
 | 1450
 AATGACCGGGCGC
 TTACTCGCCGGCG
 K * >
 458
 _____>

Figure 22A

>EcoRI_site

10	20	30	40	50	60	70	80
AAGCTTGGCTGCAGGTCGATCGACTCTAGAGGATCGATCCCCGGGAGCTCGAATTGCAACCAACCATGGTCAGCTAC							
TTCGAACCCGACGTCCAGCTAGCTGAGATCTCTAGCTAGGGGCCGCTGAGCTTAAGCGTTGGTGGTACCGAGTCGATG							
M	V	S	Y>				
1				4			

>

>BspEI_bridge

90	100	110	120	130	140	150	160
TGGGACACCGGGGCTCTGCTGTGCGCGCTCGTCAGCTGCTCTCACAGGATCTAGTCCGGAGGTAGACCTTCG							
ACCCCTGTGGCCCCAGGACGACAGCGCGACGAGTCGACAGACGAAGAGTGTCTAGATCAAGGCCATCTGGAAAGCA							
W	D	T	G	V	L	L	C
A	L	L	S	C	L	L	T
FLT1 SIGNAL SEQUENCE							
>							
S							
G>							

>

G	R	P	F	V>
				31

>

170 180 190 200 210 220 230 240

AGAGATGTACAGTCAAATCCCCGAAATTATACACATGACTGAAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTAC							
TCTCTACATGTCACTTAGGGCTTTAATATGTGACTGACTTCCTCCCTCGACCAAGTAAGGGACGGCCCAATGCAGTG							
E	M	Y	S	E	I	P	E
I	H	M	T	E	G	R	E
FLT1 IG DOMAIN 2							
>							

57

250 260 270 280 290 300 310 320

CTAACATCACTGTTACTTTAAAAAGTTTCACTTGACACTTGTGATCCCTGATGGAAAACGATAATCTGGGACAGTAGA							
GATTGAGTGACAAATGAAATTTCAAAGGTGAACGTGAAACTAGGGACTACCTTTGCGTATTAGACCCCTGTCACTCT							
P	N	I	T	V	T	L	K
K	F	P	L	D	T	L	I
FLT1 IG DOMAIN 2							
>							

84

330 340 350 360 370 380 390 400

AAGGGCTTCATCATCAAATGCAACGTACAAAGAAATAGGGCTCTGACCTGTGAAGCAACAGTCATGGCATTGTA							
TTCCCGAAGTAGTATAGTTACGTTGCATGTTCTTATCCGAAGACTGGACACTTCGTTGTCAGTTACCCGTAACAT							
K	G	F	I	I	S	N	A
T	Y	K	E	I	G	L	T
C							
E							
A							
T							
V							
N							
G							
H							
L							
Y>							

111

FLT1 IG DOMAIN 2

>

410 420 430 440 450 460 470 480

TAAGACAAACTATCTCACACATCGACAAACCAATACAATCATAGATATCCAGCTGGCCAGGAAGTCCCTGGAGCTGC							
ATTCTGTTGATAGAGTGTGAGCTGTTGGTTATGTTAGTATCTATAGGTGCAACACGGTCCTTCAGCGACCTCGACG							
K	T	N	Y	L	T	H	R
Q	T	N	I	D			
FLT1 IG DOMAIN 2							
>							

137

I Q L L P R K S L E L>

VEGFR3 (FLT4) IG DOMAIN 3

>

Figure 22B

490 500 510 520 530 540 550 560
 TGGTAGGGGAGAAGCTGGTCCCTCAACTGCACCGTGTGGGCTGAGTTAACTCAGGTGTCACCTTGACTGGGACTACCCA
 ACCATCCCTCTCGACCAGGAGTTGACGTGGCACACCCGACTCAAATTGAGTCCACAGTGGAAACTGACCCCTGATGGGT
 L V G E K L V L N C T V W A E F N S G V T F D W D Y P>
 164
 VEGFR3 (FLT4) IG DOMAIN 3 >

570 580 590 600 610 620 630 640
 GGGAAAGCAGGCAGAGCGGGGTAAGTGGGTGCCCGAGCGACGCTCCAAACAGACCCACAGAAGCTCTCCAGCATCCTGAC
 CCCTTCGTCGGTCTCGCCCCATTCAACCCACGGGCTCGCTCGAGGGTTGTCTGGGTGAGAGGTCGTAGGACTG
 G K Q A E R G K W V P E R R S Q Q T H T E L S S I L T>
 191
 VEGFR3 (FLT4) IG DOMAIN 3 >

650 660 670 680 690 700 710 720
 CATCCACAAACGTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACACGGCATCCAGCGATTTCGGGAGAGCA
 GTAGGTGTTGCAGTCGGTCGTCTGGACCCGAGCATACACAGTTCCGGTTGTCGCTAAAGCCCTCTCGT
 I H N V S Q H D L G S Y V C K A N N G I Q R F R E S>
 217
 VEGFR3 (FLT4) IG DOMAIN 3 >

730 740 750 760 770 780 790 800
 CCGAGGTCAATTGTGCATGAAAATGGCCCGGGCGACAAAACCTCACACATGCCACCGTGCCTGGCACCGACCTGAACCTCCGGGG
 GGCTCCAGTAACACGTTACCTTTACCGGGCCCGCTGTTTGAGTGTGACGGGTGGCACGGGTCTGGACTTGGAGCTTGAGGACCCC
 T E V I V H E N>
 VEGFR3 (FLT4) IG >
 G P G>
 D K T H T C P P C P A P E L L G>
 244
 FCΔC1 - A ALLOTYPE >

810 820 830 840 850 860 870 880
 GGACCGTCAGTCCTCCCTCTTCCCCCCTAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGTGCT
 CCTGGCAGTCAGAAGGAGAAGGGGGTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCA
 G P S V F L F P P K P K D T L M I S R T P E V T C V V>
 271
 FCΔC1 - A ALLOTYPE >

890 900 910 920 930 940 950 960
 GGTGGACGTGAGGCCAGAAGACCCGTAGGTCAAGTTCAACTGGTACGTGGACGGGTGGAGGTGCATAATGCCAAGACAA
 CCACCTGCACTCGGTCTGGACTCCAGTTCAAGTGTACCATGCACCTGCCGACCTCCACGTATTACGGTTCTGTT
 V D V S H E D P E V K F N W Y V D G V E V H N A K T>
 297
 FCΔC1 - A ALLOTYPE >

970 980 990 1000 1010 1020 1030 1040
 AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCCAGGACTGGCTGAATGGC
 TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGCTCTGACCGACTTACCG
 K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G>
 324
 FCΔC1 - A ALLOTYPE >

Figure 22C

1050 1060 1070 1080 1090 1100 1110 1120
 AAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCC
 TTCTCATGTTCACGGTCCAGAGTTGTTGGGAGGGTAGCTCTTTGGTAGAGGTTGGTTCCGGTCA>
 K E Y K C K V S N K A L P A P I E K T I S K A K G Q P>
 351

FCAC1 - A ALLOTYPE

>A>C_A_allotype

|>G>T_A_allotype

1130 1140 1150 1160 1170 1180 1190 1200
 CCGAGAACACAGGTGTACACCCCTGCCCATCCCGGGATGAGCTGACCAAGAACCCAGGTAGCCCTGACCTGGCTGGTCA
 GGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTCTGGTCCAGTCGGACTGGACGGGACAGT
 R E P Q V Y T L P P S R D E L T K N Q V S L T C L V>
 377

FCAC1 - A ALLOTYPE

1210 1220 1230 1240 1250 1260 1270 1280
 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACCACGCCCTCCC
 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCTCGTTACCCGTCGGCCTTGTGATGTTCTGGTCCGGAGGG
 K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P>
 404

FCAC1 - A ALLOTYPE

>T>C

1290 1300 1310 1320 1330 1340 1350 1360
 GTGCTGGACTCCGACGGCTCCTCTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTT
 CACGACCTGAGGCTGCCAGGAAGAAGGAGATATCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCCTGAGAA
 V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F>
 431

FCAC1 - A ALLOTYPE

>NotI_site

1370 1380 1390 1400 1410 1420 1430 1440
 CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAGAGCCTCTCCCTGTCCTGGGTAATGAGCGG
 GAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTAGTGTGCGTCTCTCGGAGAGGGACAGAGGCCATTACTCGCC
 S C S V M H E A L H N H Y T Q K S L S L S P G K *>
 455

FCAC1 - A ALLOTYPE

CCGC
 GGCG

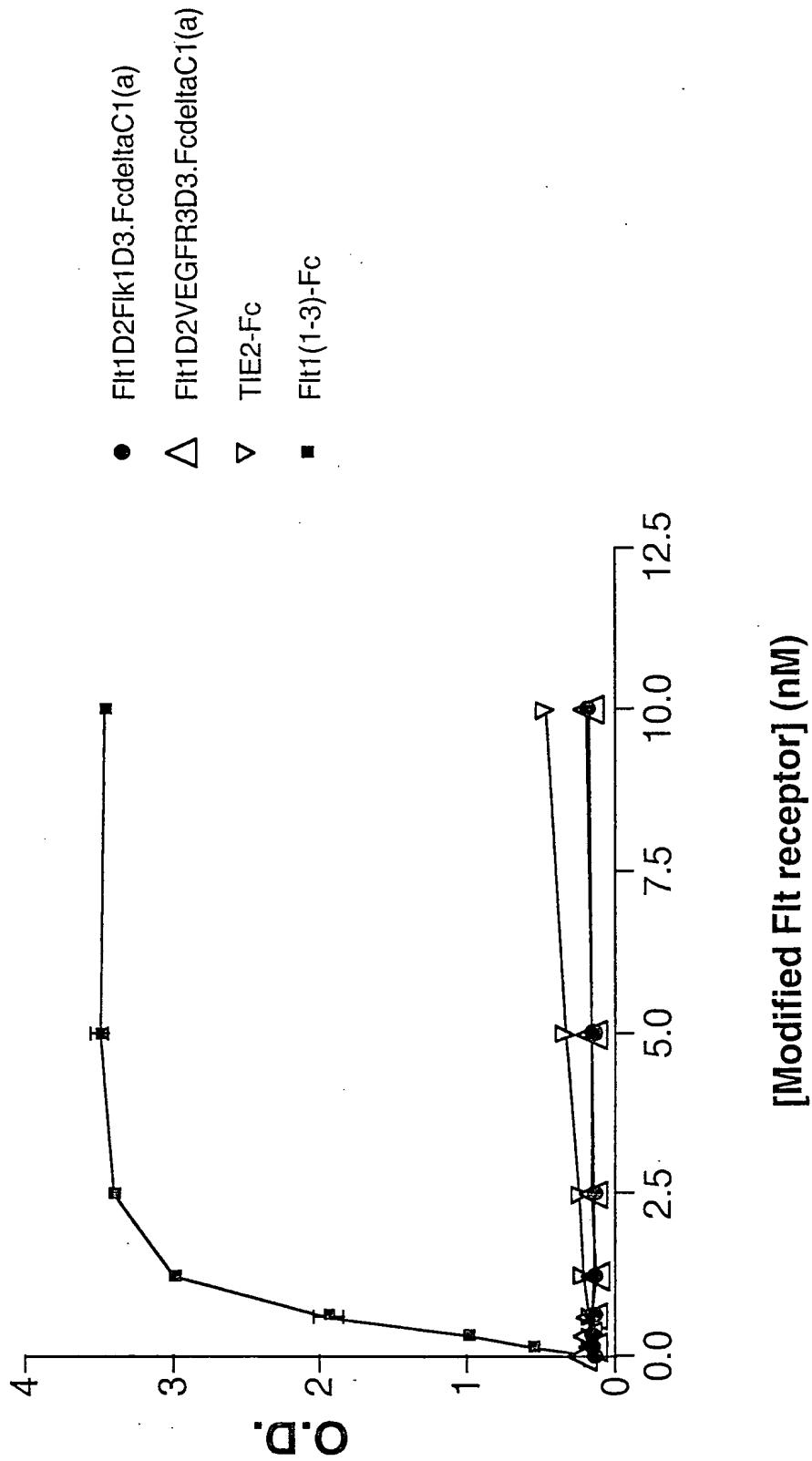
Figure 23

Figure 24A

TOPPED-223E/260

10	20	30	40	50	60
* *	* *	* *	* *	* *	* *
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC					
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC CGC GAC GAG TCG ACA GAC GAA GAG					
M V S Y W D	T G V L L C	A L L S C L	L L S C L L	L>	L>
1	5	hFLT1 SIGNAL SEQUENCE	15	20	20>

70	80	90	100	110	120
* *	* *	* *	* *	* *	* *
ACA GGA TCT AGT TCC GGA AGT GAT ACC GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC					
TGT CCT AGA TCA AGG CCT TCA CTA TGG CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG					
T G S S S G>	21_hFLT1 SIGNAL SEQ_26>				

27	30	hFLT1	IG DOMAIN 2	40>	
S D T G R P F V E M Y S E I>					

130	140	150	160	170	180	
* *	* *	* *	* *	* *	* *	
CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA						
GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT						
P E I I H M T E G R E L V I P C R V T S>	41	45	hFLT1	IG DOMAIN 2	55	60>

190	200	210	220	230	240	
* *	* *	* *	* *	* *	* *	
CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA						
GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT						
P N I T V T L K K F P L D T L I P D G K>	61	65	hFLT1	IG DOMAIN 2	75	80>

250	260	270	280	290	300	
* *	* *	* *	* *	* *	* *	
CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA						
GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT						
R I I W D S R K G F I I S N A T Y K E I>	81	85	hFLT1	IG DOMAIN 2	95	100>

310	320	330	340	350	360	
* *	* *	* *	* *	* *	* *	
GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA						
CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT						
G L L T C E A T V N G H L Y K T N Y L T>	101	105	hFLT1	IG DOMAIN 2	115	120>

370	380	390	400	410	420	
* *	* *	* *	* *	* *	* *	
CAT CGA CAA ACC AAT ACA ATC ATA GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT GAA CTA						
GTA GCT GTT TGG TTA TGT TAG TAT CTA CAC CAA GAC TCA GGC AGA GTA CCT TAA CTT GAT						
H R Q T N T I I D>	121	129	hFLT1	IG DOMAIN 2	129	

130	hFLT1	IG DOMAIN 3	140>
V V L S P S H G I E L>			

Figure 24B

ROTETO-22854260

430	440	450	460	470	480				
*	*	*	*	*	*				
TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA AAT GTG GGG ATT									
AGA CAA CCT CTT TTC GAA CAG AAT TTA ACA TGT CGT TCT TGA CTT GAT TTA CAC CCC TAA									
S V G E K L V L N C T A R T E L N V G I>									
141	145	hFLK1 IG DOMAIN 3			155				
160>									
490	500	510	520	530	540				
*	*	*	*	*	*				
GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG AAA CTT GTA AAC CGA GAC									
CTG AAG TTG ACC CTT ATG GGA AGA AGC TTC GTA GTC GTA TTC TTT GAA CAT TTG GCT CTG									
D F N W E Y P S S K H Q H K K L V N R D>									
161	165	hFLK1 IG DOMAIN 3			175				
180>									
550	560	570	580	590	600				
*	*	*	*	*	*				
CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT TTG AGC ACC TTA ACT ATA GAT GGT									
GAT TTT TGG GTC AGA CCC TCA CTC TAC TTC TTT AAA AAC TCG TGG AAT TGA TAT CTA CCA									
L K T Q S G S E M K K F L S T L T I D G>									
181	185	hFLK1 IG DOMAIN 3			195				
200>									
610	620	630	640	650	660				
*	*	*	*	*	*				
GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG									
CAT TGG GCC TCA CTG GTT CCT AAC ATG TGG ACA CGT CGT AGG TCA CCC GAC TAC TGG TTC									
V T R S D Q G L Y T C A A S S G L M T K>									
201	205	hFLK1 IG DOMAIN 3			215				
220>									
670	680	690	700	710	720				
*	*	*	*	*	*				
AAG AAC AGC ACA TTT GTC AGG GTC CAT GAA AAG GAC AAA ACT CAC ACA TGC CCA CCG TGC									
TTC TTG TCG TGT AAA CAG TCC CAG GTC CTT TTC CTG TTT TGA GTG TGT ACG GGT GGC ACG									
K N S T F V R V H E K>									
221	hFLK1 IG DOMAIN 3			231	>				
232	D	K	T	H	T	C	P	P	C>
									240>
730	740	750	760	770	780				
*	*	*	*	*	*				
CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC									
GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG									
P A P E L L G G P S V F L F P P K P K D>									
241	245	hFCAC1 A			255	260>			
790	800	810	820	830	840				
*	*	*	*	*	*				
ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC GAA									
TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT									
T L M I S R T P E V T C V V V D V S H E>									
261	265	hFCAC1 A			275	280>			
850	860	870	880	890	900				
*	*	*	*	*	*				
GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA									
CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTC TTA CGG TTC TGT									
D P E V K F N W Y V D G V E V H N A K T>									
281	285	hFCAC1 A			295	300>			

Figure 24C

DRAFT 2/28/2000

910	920	930	940	950	960
*	*	*	*	*	*
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG					
TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC					
K P R E E Q Y N S T Y R V V S V L T V L>					
301	305	hFCAC1 A	315	320	
970 980 990 1000 1010 1020					
*	*	*	*	*	*
CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA					
GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT					
H Q D W L N G K E Y K C K V S N K A L P>					
321	325	hFCAC1 A	335	340	
1030 1040 1050 1060 1070 1080					
*	*	*	*	*	*
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC					
CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG					
A P I E K T I S K A K G Q P R E P Q V Y>					
341	345	hFCAC1 A	355	360	
1090 1100 1110 1120 1130 1140					
*	*	*	*	*	*
ACC CTG CCC CCA TCC CCG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC					
TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TIG GTC CAG TCG GAC TGG ACG GAC CAG					
T L P P S R D E L T K N Q V S L T C L V>					
361	365	hFCAC1 A	375	380	
1150 1160 1170 1180 1190 1200					
*	*	*	*	*	*
AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC					
TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG					
K G F Y P S D I A V E W E S N G Q P E N>					
381	385	hFCAC1 A	395	400	
1210 1220 1230 1240 1250 1260					
*	*	*	*	*	*
AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG					
TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC					
N Y K T T P P V L D S D G S F F L Y S K>					
401	405	hFCAC1 A	415	420	
1270 1280 1290 1300 1310 1320					
*	*	*	*	*	*
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT					
GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTC					
L T V D K S R W Q Q G N V F S C S V M H>					
421	425	hFCAC1 A	435	440	
1330 1340 1350 1360 1370					
*	*	*	*	*	*
GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA					
CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT					
E A L H N H Y T Q K S L S L S P G K *>					
441	445	hFCAC1 A	455	458	>

Figure 25B

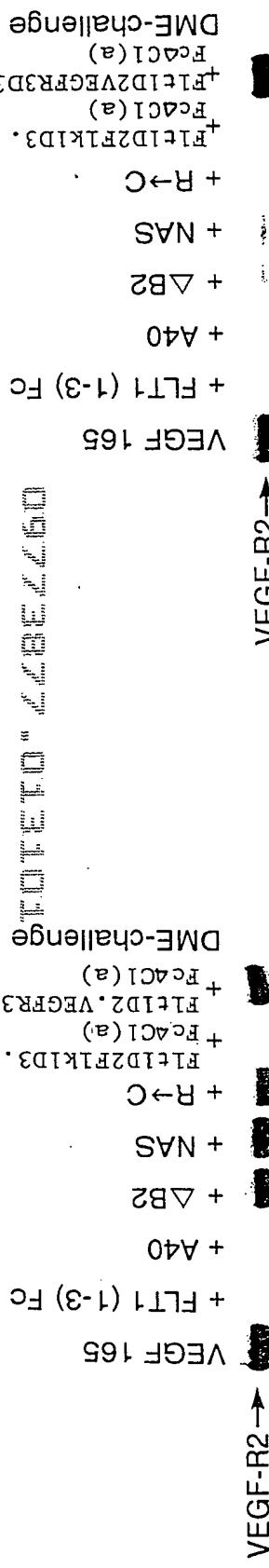


Figure 25A

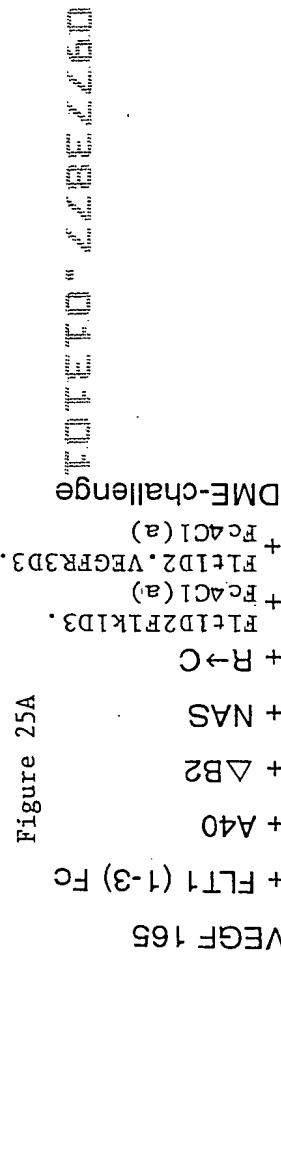
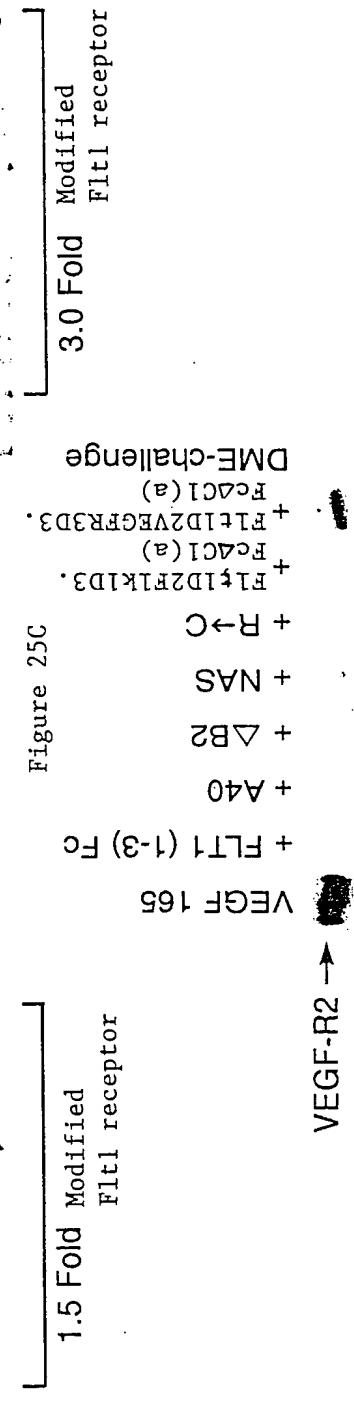


Figure 25C



6.0 Fold Modified Fltl receptor

Figure 26A
Figure 26B

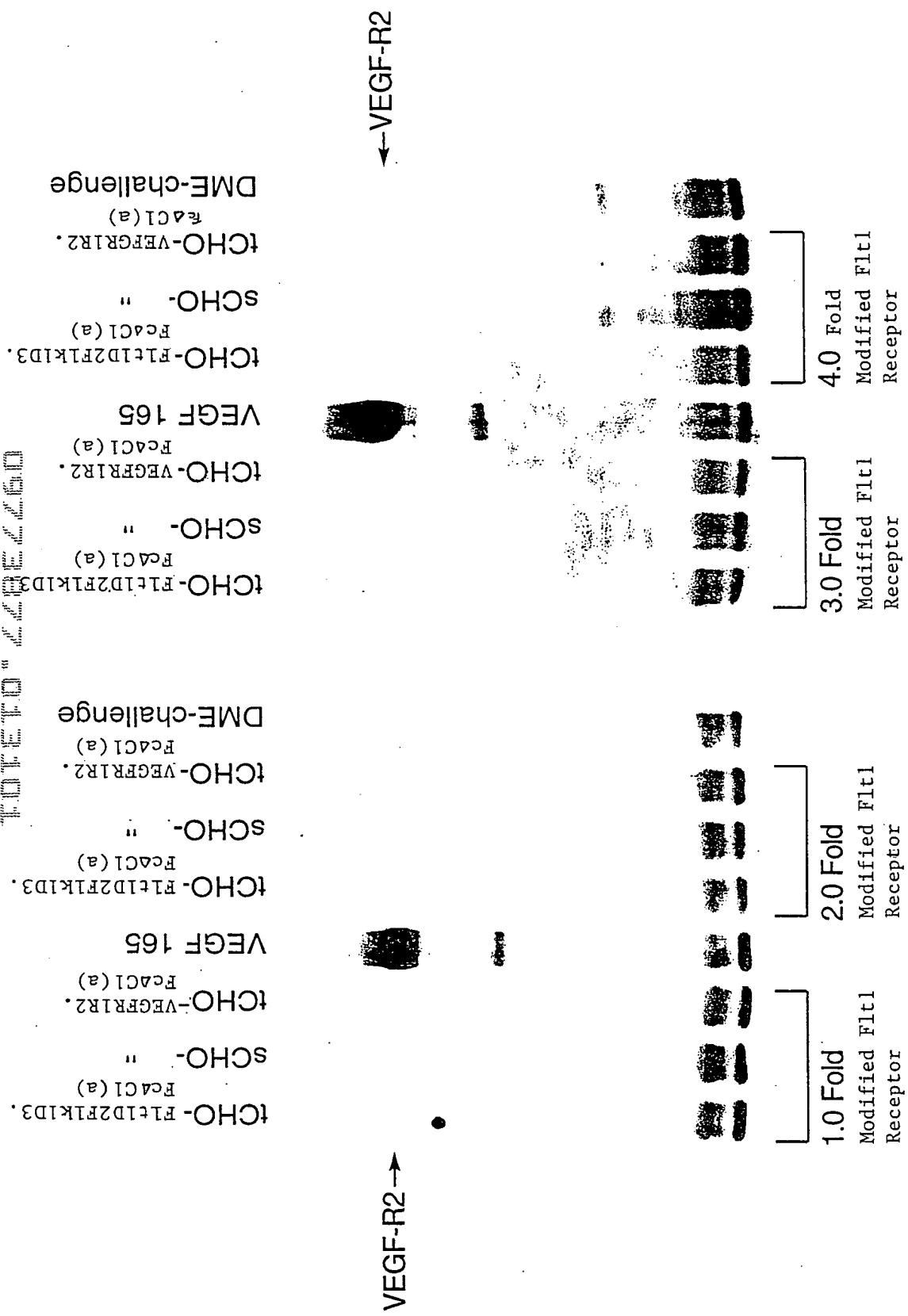


Figure 27

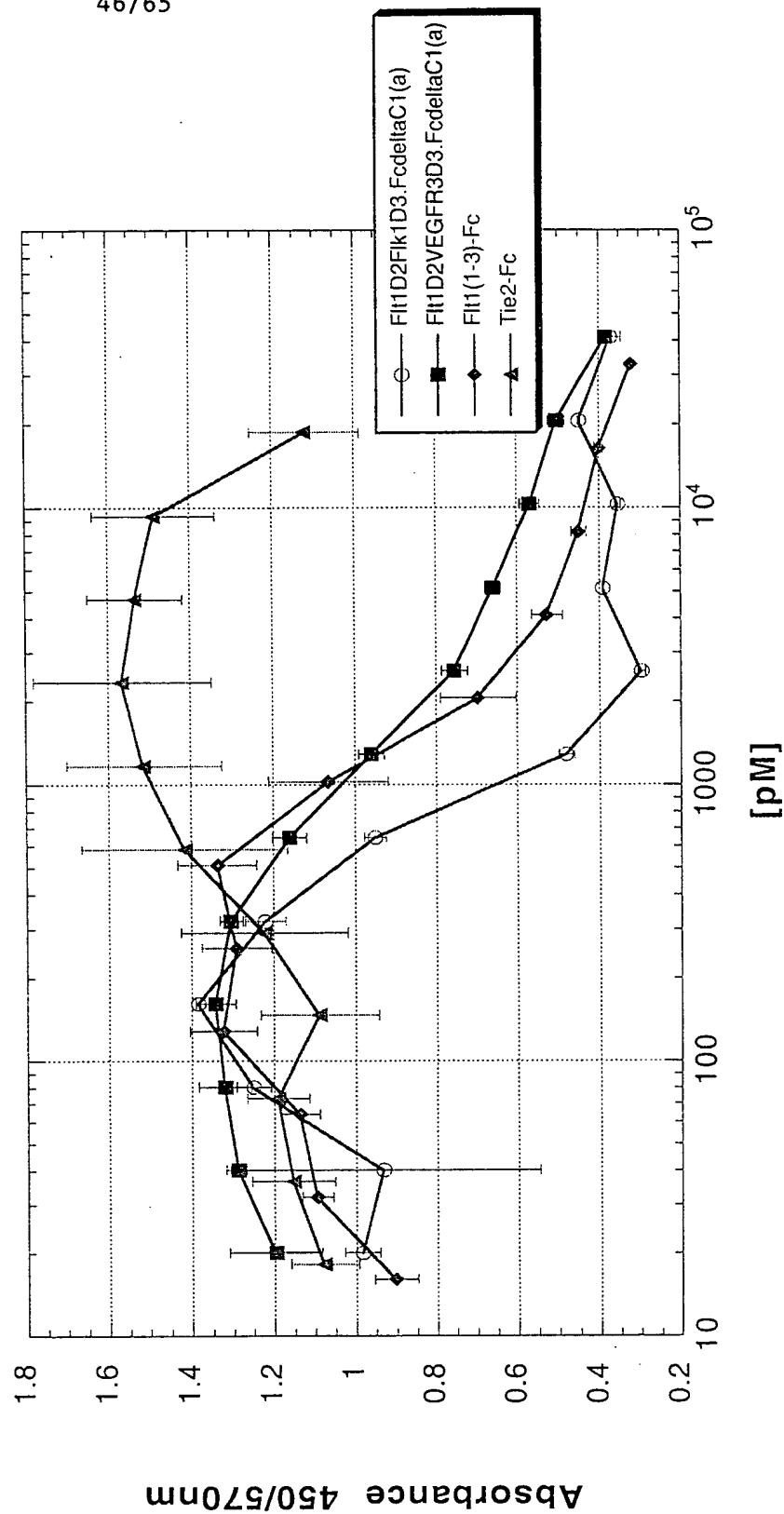


Figure 28

Binding Stoichiometry of hVEGF165 to F1t1D2F1k1D3.Fc α C1 (a) & VEGFR1R2-Fc α C1 (a)		
hVEGF165 (nM)	VEGF/F1t1D2F1k1D3.Fc α C1 (a)	VEGF/VEGFR1R2-Fc α C1 (a)
1	0.93	0.98
10	0.97	0.94
50	1	0.99
Average \pm StDev	0.96 \pm 0.03	0.97 \pm 0.02

Figure 29

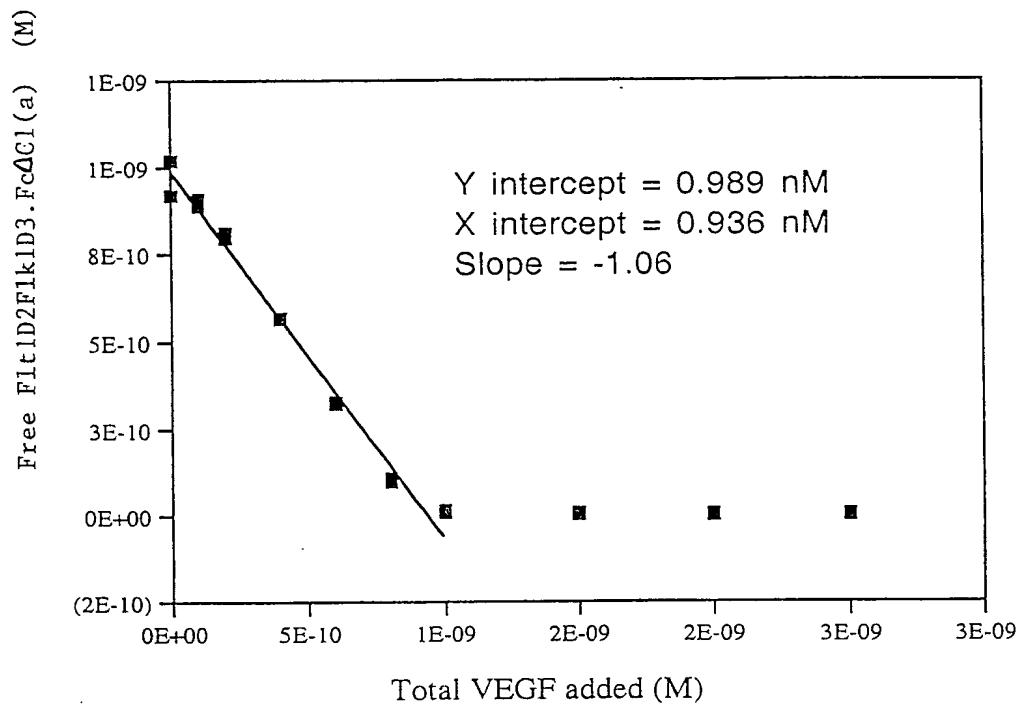


Figure 30

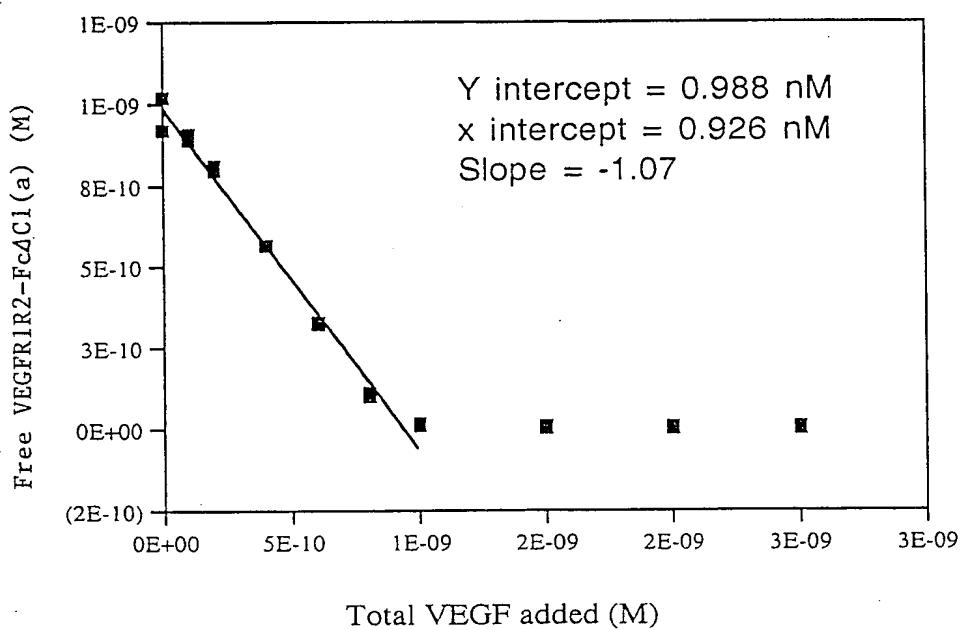


Figure 31

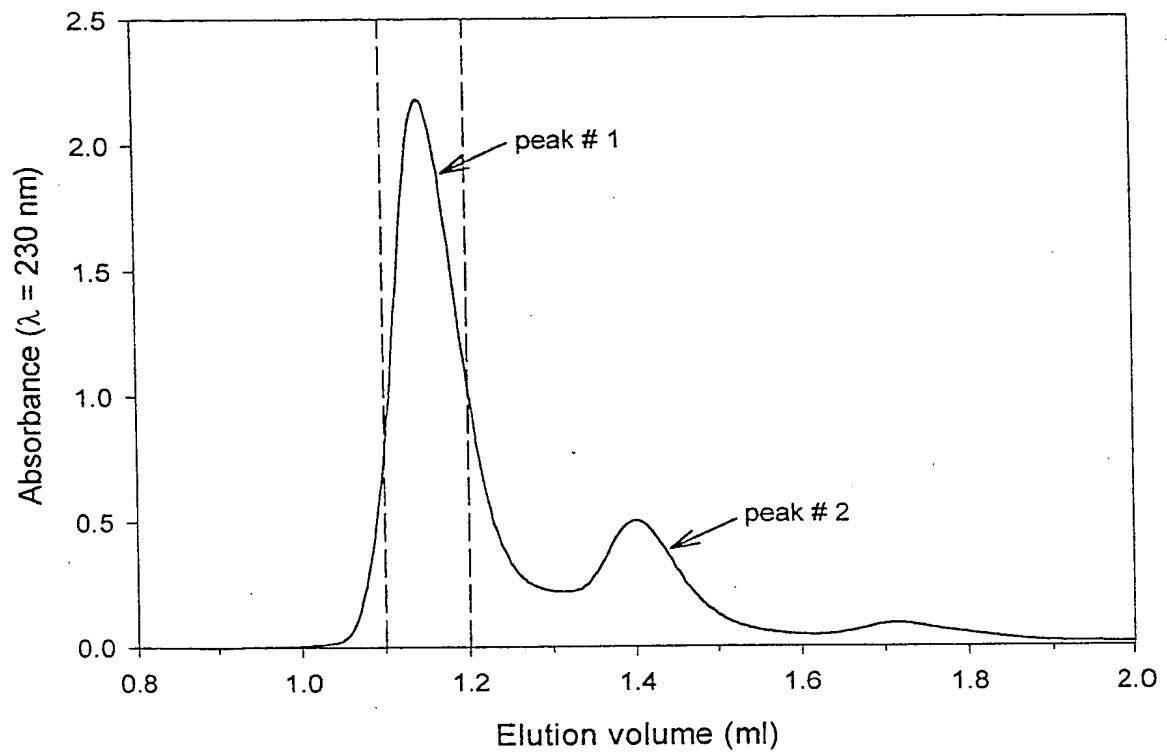


Figure 32

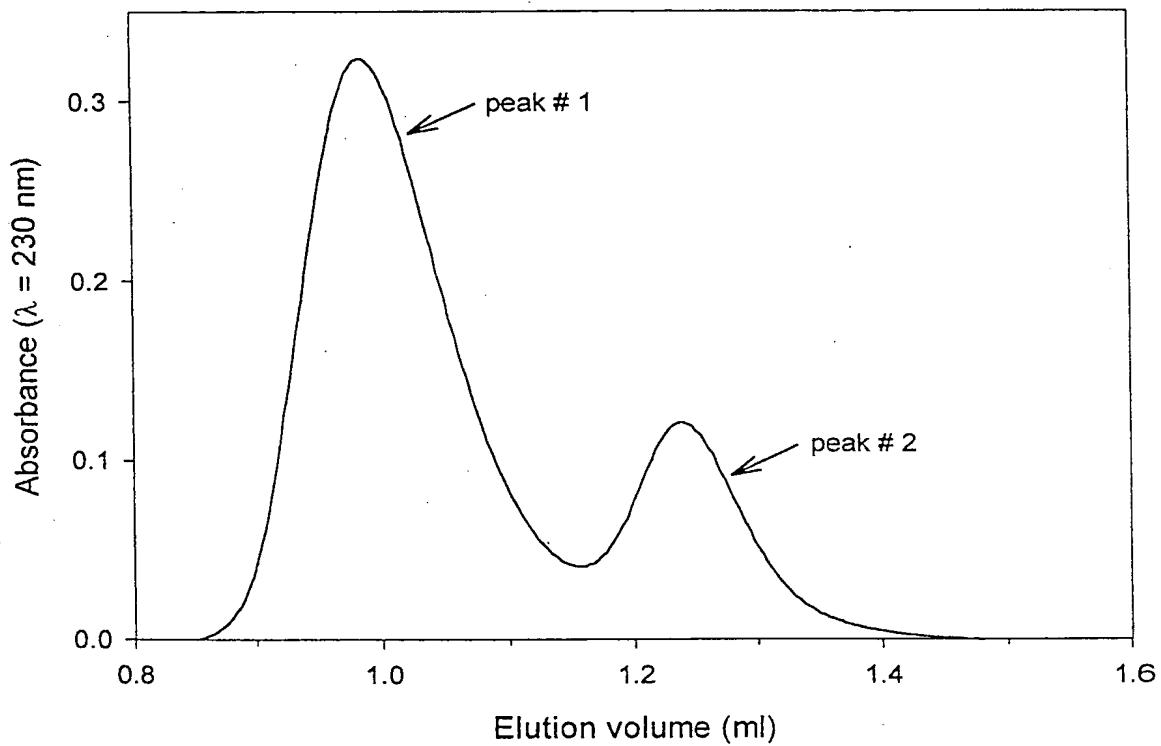


Figure 33

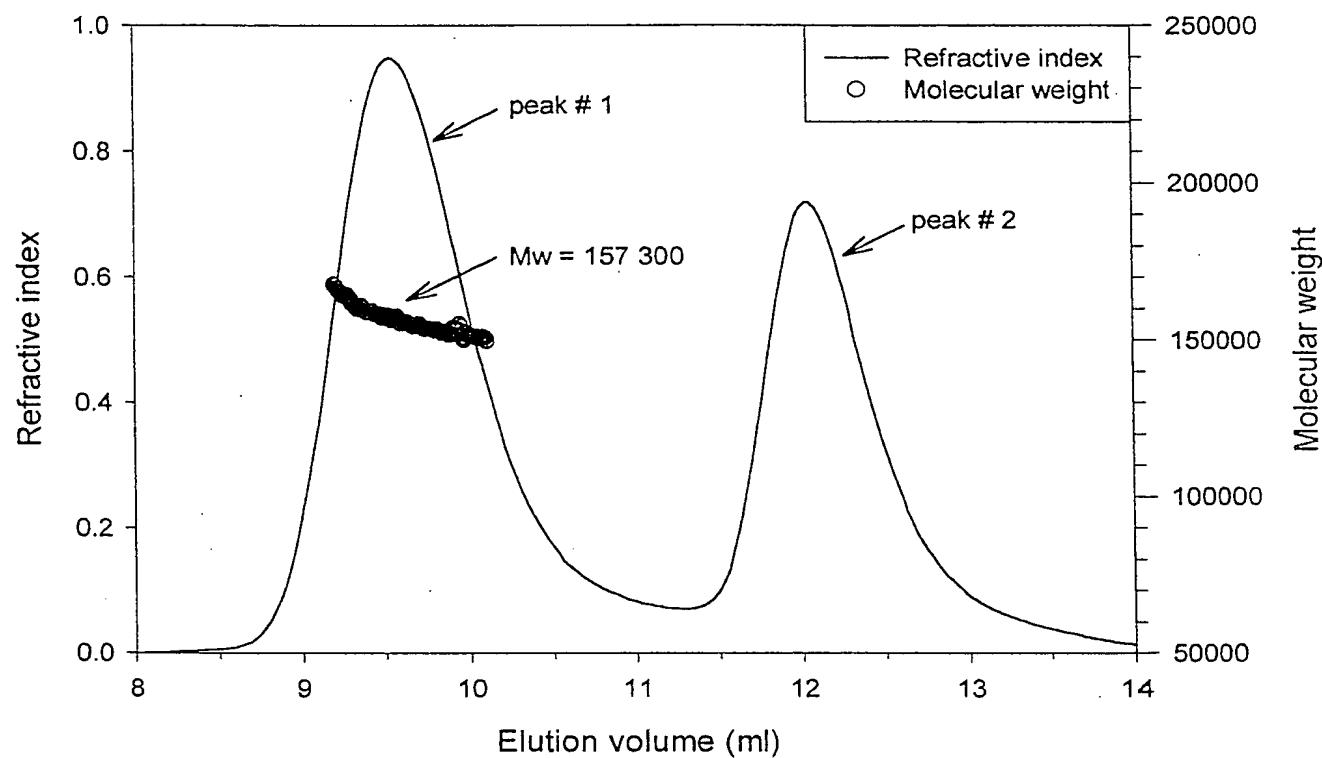


Figure 34

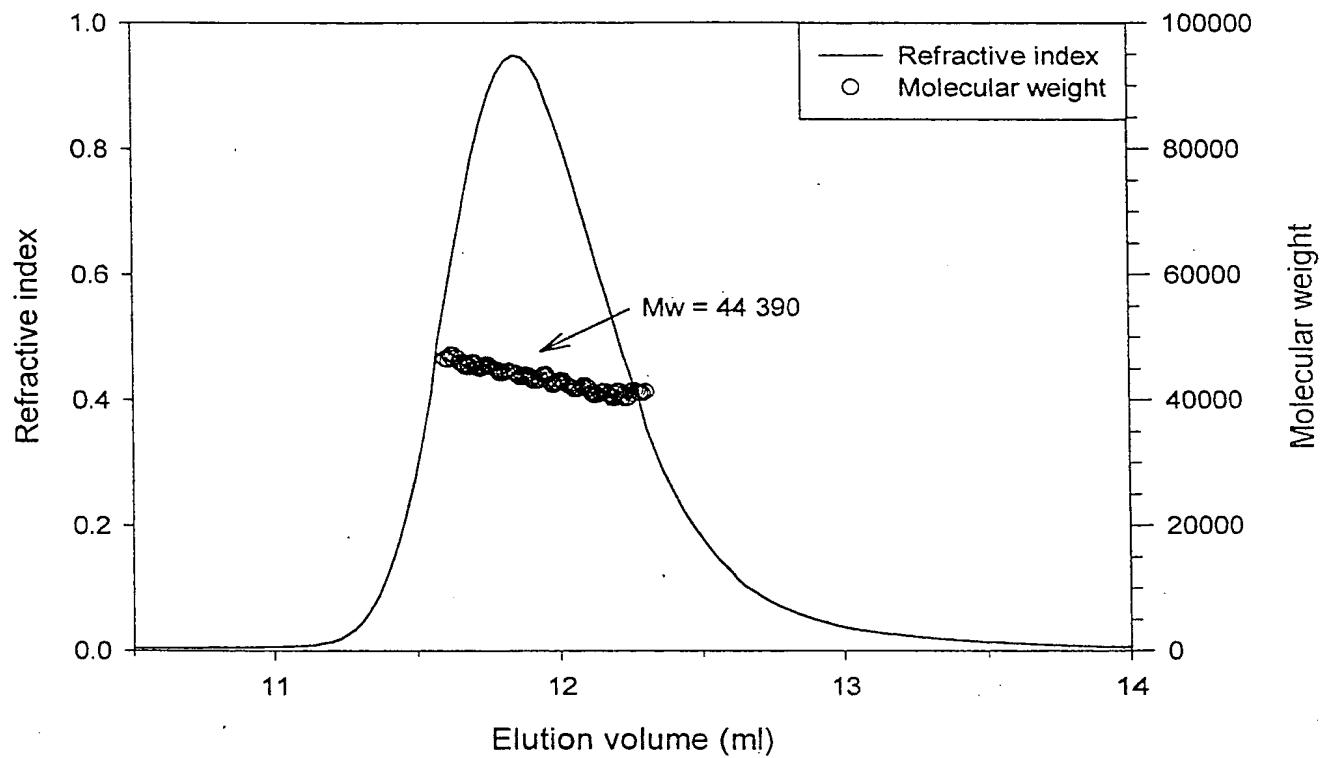


Figure 35

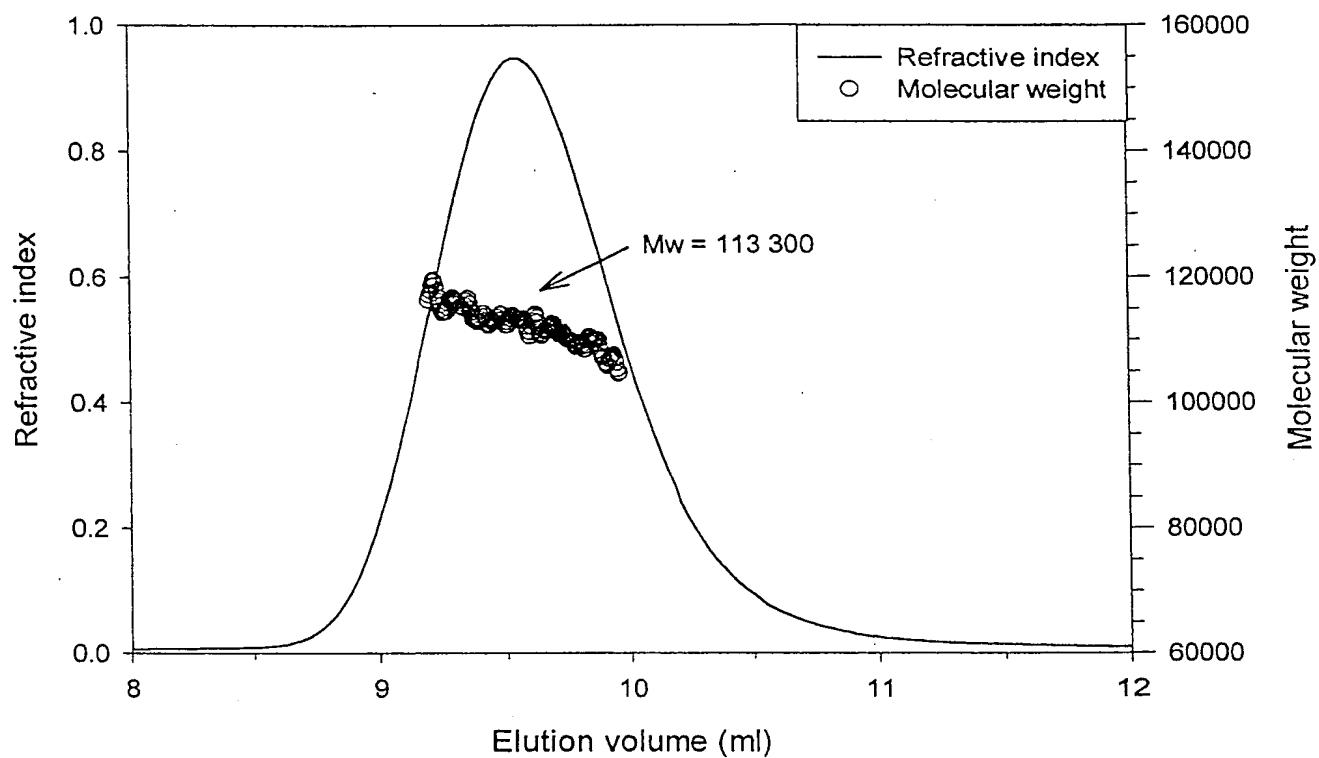


Figure 36

GRPFVEMYSEIPEIHMTEGRELVIPPCRVTSPNITVTLKKFPLDTLIPDG
 KRUIWDSRKGFISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTID
 VVLSPSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHHQHKKLVNR
 DLKTQSGSEMKKFLSTLTTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVH
 EKGPGDKTTHTCPPCPAPELLLGGPSVFLFPKPKDTLMISRTPEVTCVVVD
VSHEDPEVKFNWYVDGVEVHNAAKTKPREEQYNSTYRVVVSVLTVLHQDWLN
 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
 TCLVKGFYPSDIAVEWESNGQOPENNYKRTTPVLDSDGSFFLYSKLTVDKS
 RWQQGNVFSCSVMHEALHNHYTQKSLSSPGK

Figure 37

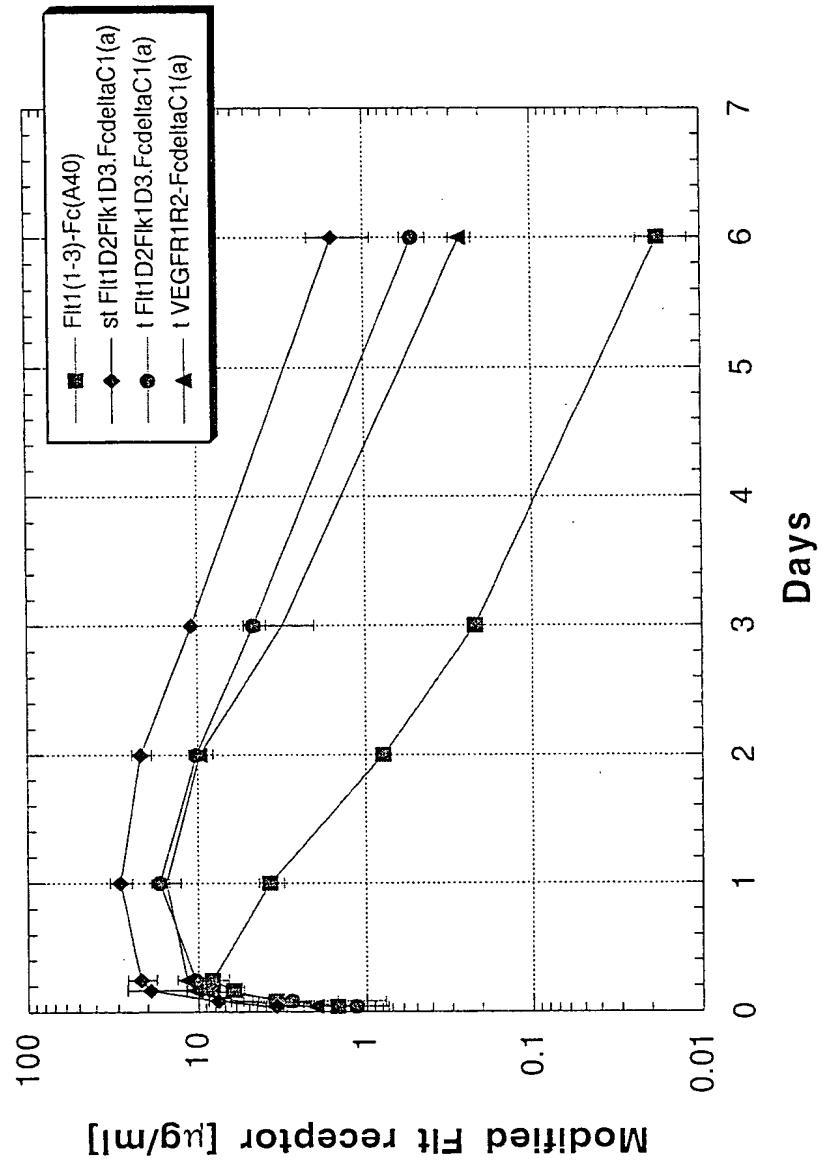


Figure 38

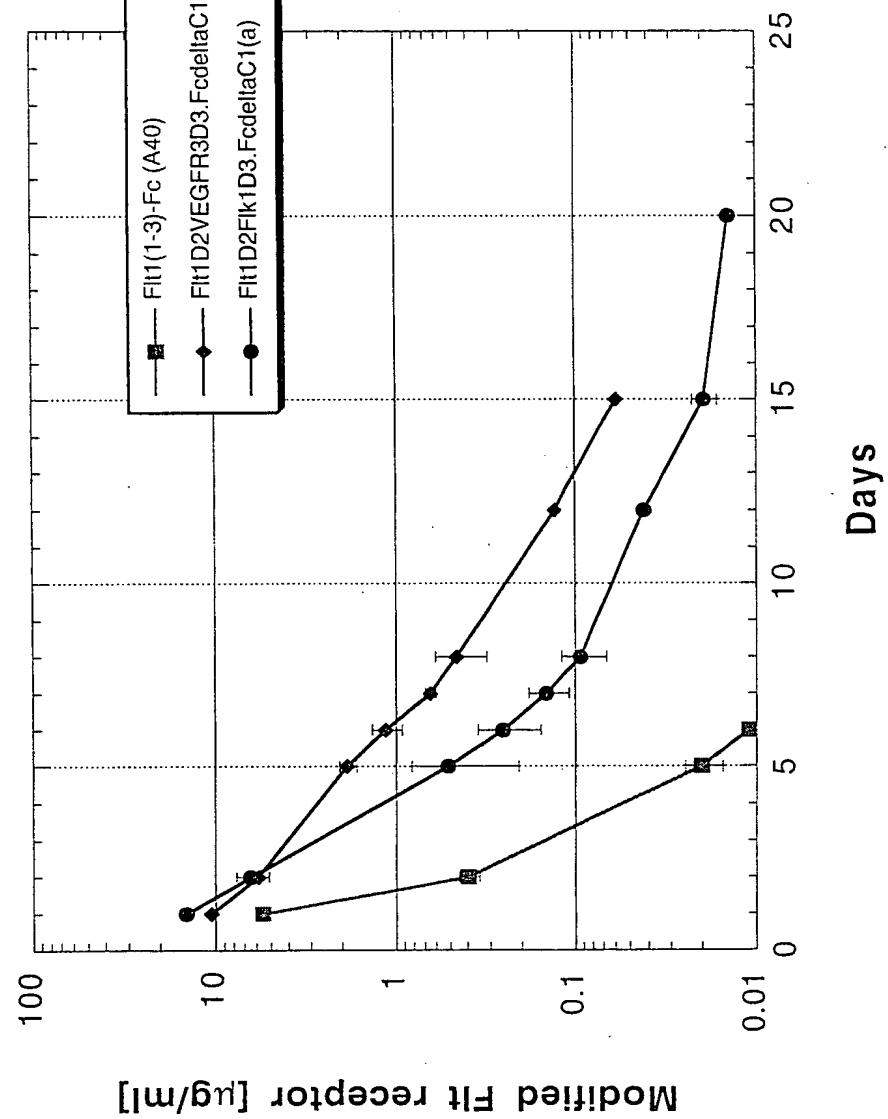


Figure 39

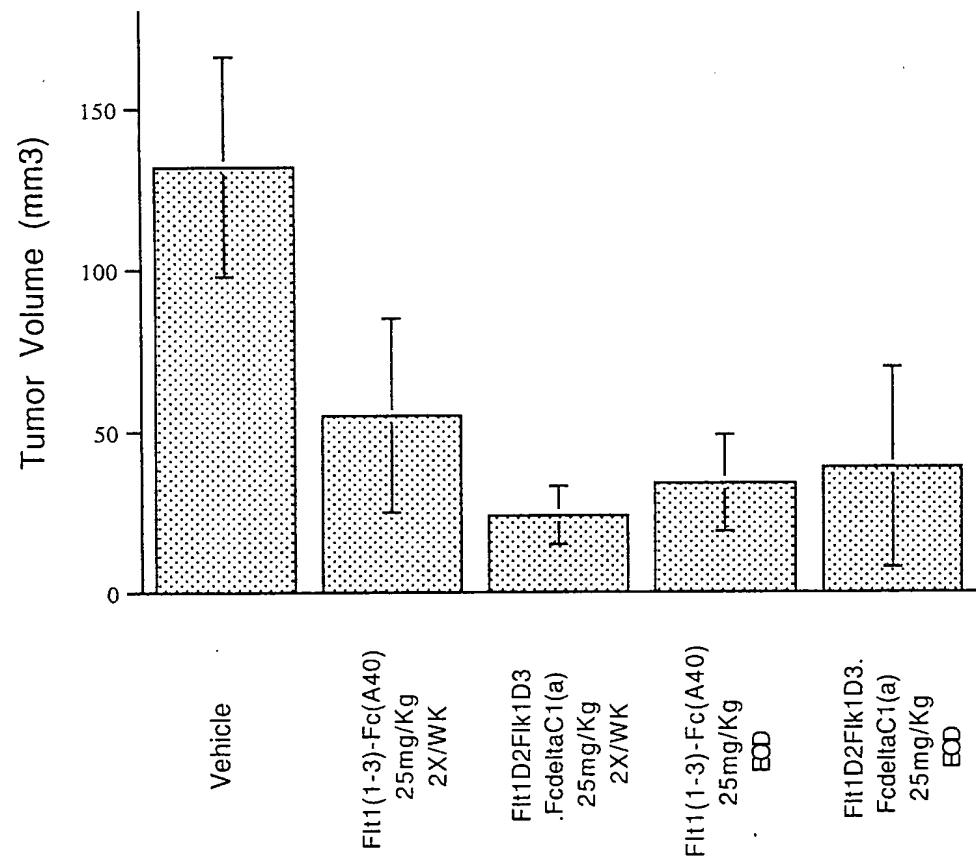


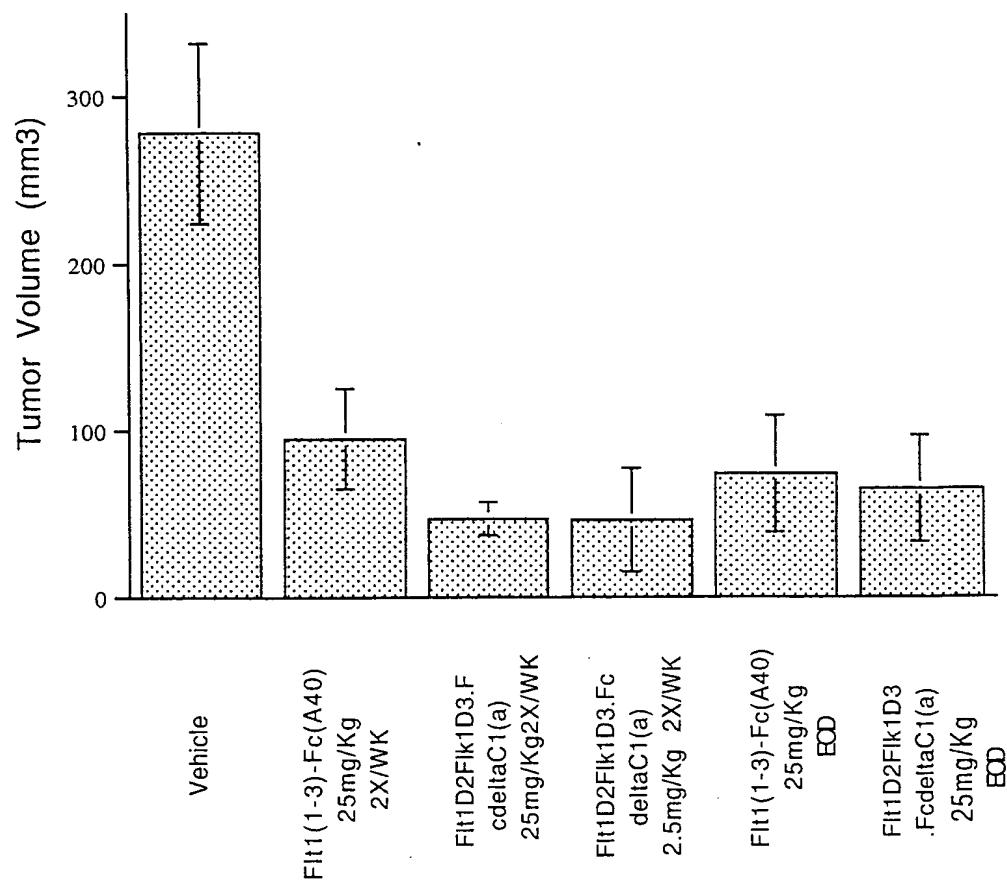
Figure 40

Figure 41

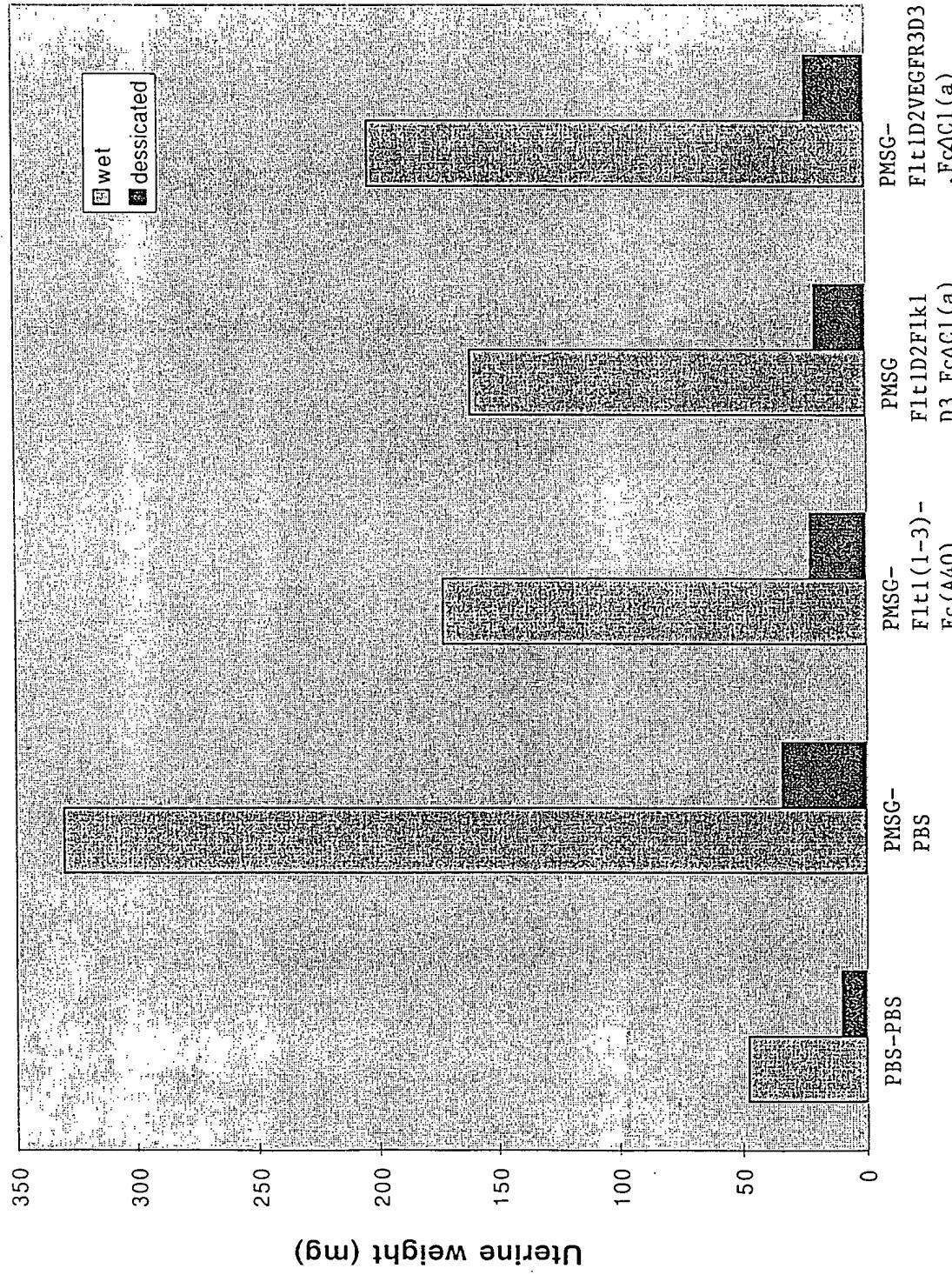


Figure 42A

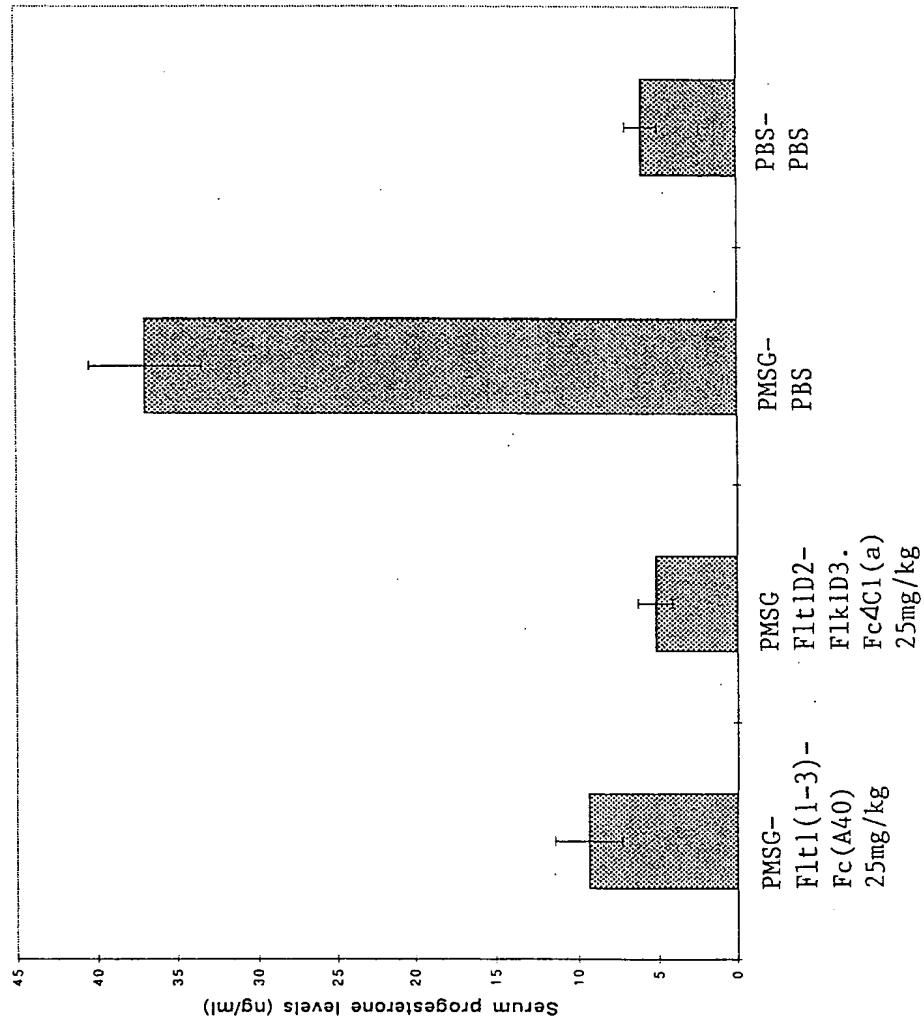


Figure 42B

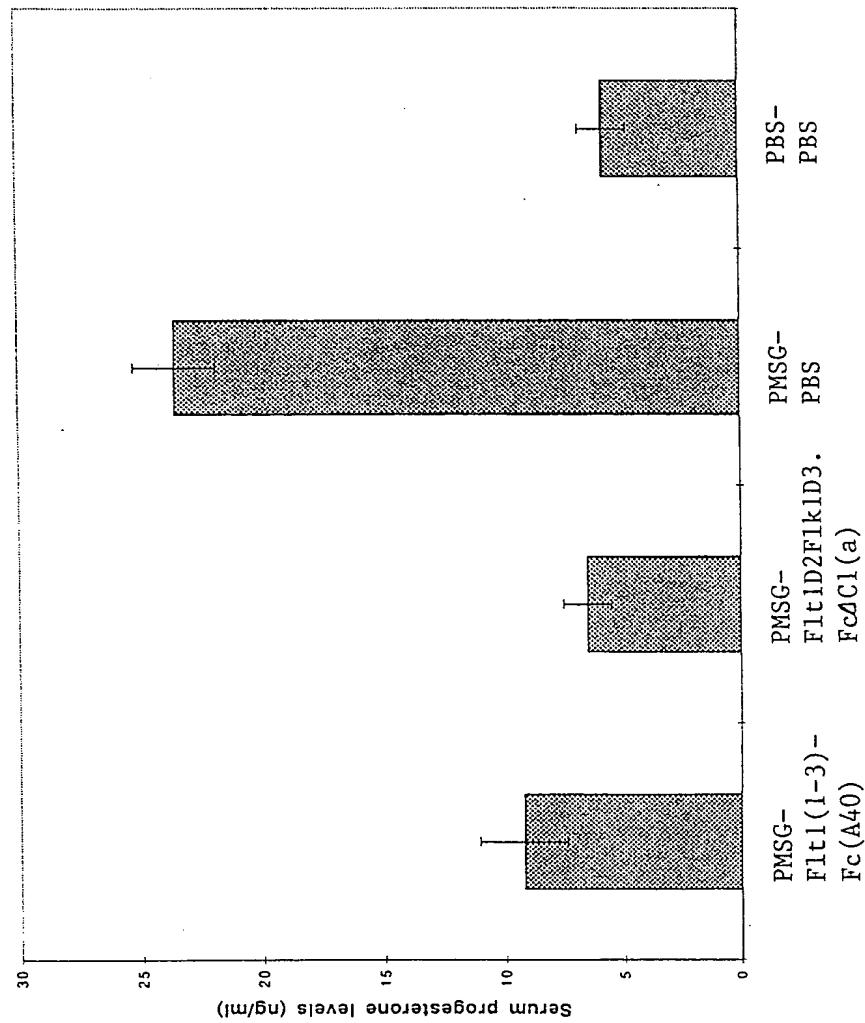


Fig.43

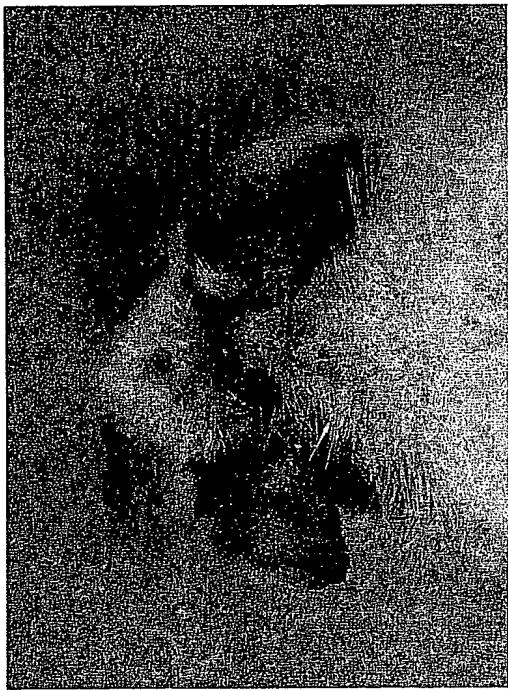


Fig.44A

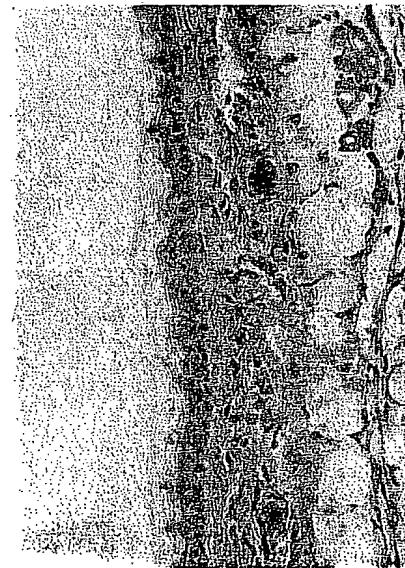


Fig.44 B

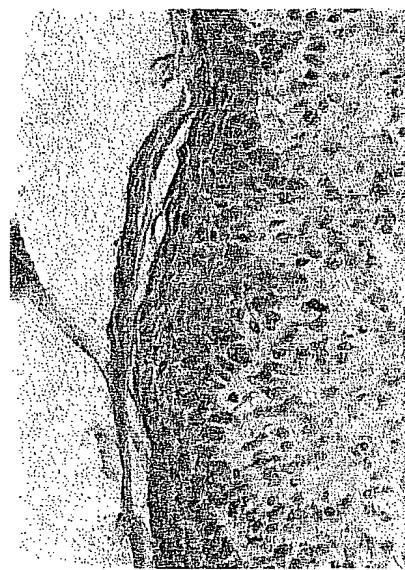


Fig.44 B

Fig.44 C



Fig.45



Fig.46 A-B

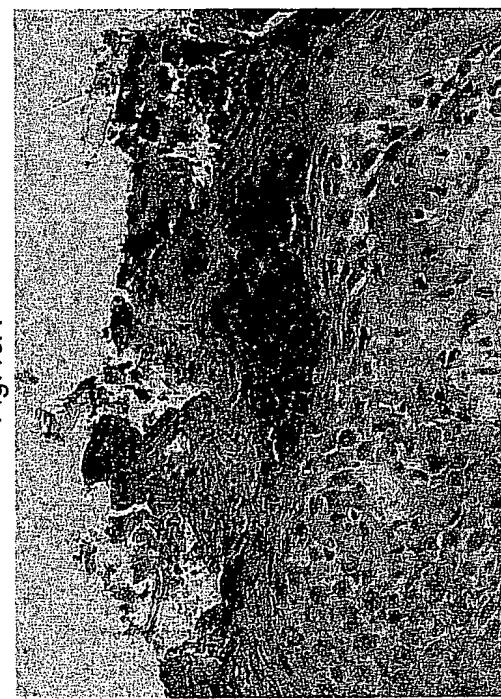


Fig.46B



